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OW nucleic - nucleic search, using sw model

Run on: June 1, 2003, 23:40:52 ; Search time 292 Seconds
(without alignments)
7288.145 Million cell updates/sec

Title: US-09-978-274A-1
Perfect score: 945
Sequence: 1 atgaaggtatctgttagt.....atctattgaaggattctaa 945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632.4	66.9	1379	21	AAZ59220 pokeweed antiviral
2	632.4	66.9	1379	21	AAZ45197 Wild-type pokeweed
3	630.8	66.8	1195	15	AAQ56672 Sequence of Phyto
4	630.8	66.8	1379	22	AAC87929 P. americana pokew
5	629.2	66.6	1195	16	AAQ81457 Phytoactin antivir
6	629.2	66.6	1379	21	AAZ59221 Variant pokeweed a
7	624.2	66.2	1472	14	AAQ43967 pokeweed insular
8	588.6	62.3	882	19	AAQ99556 Phytoactin insular
9	586.4	62.1	2369	19	AAQ99557 Phytoactin insular

06/02/2003

Phytoactin insular
Antiviral protein
DNA pJMC201 fragme
Wild-type pokeweed
Cloning vector pR1
DNA of ribosome I
Saporin coding seq
M13mpl8-G2, a sapor
M13mpl8-G9, a sapor
Saporin clone M13
Saporin cDNA clone
Saporin cDNA clone
Saporin cDNA clone
Saporin cDNA clone
Gelatin toxin DNA
DNA encoding a sap
DNA encoding chemo
DNA encoding chemo
DNA encoding chemo
Saporin coding seq
M13mpl8-G1, a sapor
Saporin clone M13
Saporin cDNA clone
VEGPI65-AtMeth-SAP
Saporin coding seq
Saporin coding seq
M13mpl8-G4, a sapor
M13mpl8-G2, a sapor
Saporin clone M13
Saporin clone M13

ALIGNMENTS

RESULT 1
AAZ59220 standard: cDNA: 1379 BP.
AAZ59220:

20-APR-2000 (first entry)

Pokeweed antiviral protein coding sequence spring leaf form.

Pokeweed antiviral protein spring leaf form; PAP: transgenic plant;
Resistance; Potato virus X; potato virus Y; potato leaf roll virus;
tuber; ss.

Phytoactin americana.

US6015940-A.

18-JAN-2000.

07-APR-1992: 92US-0865169.

07-APR-1992: 92US-0865169.

(MUNS) MONSANTO CO.

Koniewski WK, Turner NE, Lodge JK.

WPI: 2000-126326/11.

Production of transgenic potato plants or tubers expressing pokeweed
antiviral protein which are resistant to potato virus X or Y.

Query Match	66.9%	Score 632.4	DB 21	Length 1379	
Best Local Similarity	80.0%	Ident. No. 21e-166			
Matches 757	Conservative	0	Mismatches 186	Indels 3	Gaps 1
3	GAAGGTGATGCTTGTAGTTTGTGTGACGTTAATACGCTGGCTCATTTGCTGCACCAACTTC	62			
221	GAAGATGAAGTCGATCGTGTGGTGACAAATATCAATATGCGCTCATCTTTGCCACCAACTTC	280			
63	AACCTTGGCATAAATACGATCACCCTTTCGATGCTGGAAATGCCACCATTAACAANAATATGC	122			
281	AACCTTGGGCTTGAATACAAATCATCTACAAATGTTGGAAGTACCAACATATAGCAAAATACGC	340			
123	CACCTTTATGGAAATCTCTTCTGAATCAACGCGAAAGATCCAAAACTFAAAATGCTATGGCAT	182			
341	CACCTTTCTGAATGATCTTCGTAATGAACGGAAGATCCAAAGTTTAAATGCTATGGAAAT	400			
183	ACCAATGCTACCTGATACATAATTCGACCCCTTAAGTACTTATTTGGTTAAGCTCCAAGTGC	24			
401	ACCAATGCTGCCCAATACAAATACAAATACAAATCCAAAGTACGTTTGGTTACAGCTCCAAGTTC	460			
243	AAACCTAAAAACCATTAACACTTAATGCTGAGACGAATAACTTATACGTTATGCGGTATTC	302			
461	AATAAAAAACCATCACACTAATGCTGAGACGAACAAATTTGTTATGTTGGGTATTC	520			
303	TGATCCCTTCAATGGCAATAAAGTGTGGTTACCATATATTTAATGATATTACAAGCACCGA	362			
521	TGATCCCTTTGAACCAATAAATGCTGTACCATATCTTTAATGATATCTCAGGTACTGA	580			
363	ACGCACCTGATGGGCAATACCTTTTGGCTCAAGTTCTAGTTCTCGTGTTGCAATGTCAT	422			
581	ACGCCAAGATGTAGAGACTACTCTTTGCCCAATGCCAATCTCTCGTTGTTAAGAAATCA	640			
423	TAACATAAATAGCTTATATCCGACCATGGAAGAAAGCAAGAACTAACTCAAGAAATCA	482			
641	AAACTTTGATAGTCGATATCCAAACATTTGGAATCAAAAGCGGAGTAAAAATCAAGAATCA	700			
483	AGTCCCAATGGGAATTCAAATACACGACGATCAGATTCGGAATAATCTCTGAGTTGATTC	542			
701	GGTCCCACTGGGAATTCAAATACTCACAGTAAATTTGGAAGATTTCTGGAGTGTATGTC	760			
543	ATTCCCTGTAAAACTACGCGCTTTTTCCTACTGTTAGCCATCCCAATTCGTTTCAGAGGC	602			
761	ATTCACTGAGAAACCGGAGCGGAATTCCTATTTGTTAGCCATACAAATGTTATCAGAGGC	820			
603	AGCGGATTCACGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGACCATTTCAACC	662			
821	AGCAAGATTCAGTACATAGAGAACTAGGTGAAACTAATTTTAAACAGGCTTCAACACC	880			
663	TGATCCCAAGTAAATTAATTTGGAGGAGAGTGGGGCAAAATCTCTGAGGCAATTCACAA	722			
881	TAATCCCAAGTAACTTAATTTGCAAGAGACATGGGGTAAAGATTTCAACAGCAATTCATGA	940			
723	TGCCAAGATGGGGCTTTACCCAAACCACTTCAGCTACTGGATGCCAAGGTACCAAGTC	782			
941	TGCCAAGATGGAGTTTAAACCAACCTTCAGCTAGTCGATGCCAGTGGTGGCCAAGTC	1000			
783	GATAGTTCTTAGAGTGGATGAATCAATCGTGATGTGGCACTCTTAAGTACGTTAATGG	842			
1001	GATAGTGTGTGAGAGTGCATGAATCAAGGCTCATGTATGATGCTTCTTAAGTACGTTAATGG	1060			
843	AACCTGTGCAGACAACCTTACCAAAATGCCATGTTCTCAAGTATAATTTTCACTTA	899			
1061	GAGCTGTGCAGACAACCTTATAACCAAAATGCCATGTTCTCTCACTTATATGTCCTACTTA	1120			
900	TTATAATATATGTCTAAATCTTGGTGATCTATTTGAAGGATTTCTAA	945			
1121	TTATAATATATGTCTAAATCTTGGTGATCTATTTGAAGGATTTCTGA	1160			

RESULT 3
AAQ56672
IID AAQ56672 standard; CNA; 1195 BP.

Printed: 11/17/2004

SRNT

09978274

AAZ59221 standard: cDNA; 1379 BP.
AAZ59221:
20-APR-2000 (first entry)
Variant pokeweed antiviral protein spring leaf form coding sequence.
Pokeweed antiviral protein spring leaf form: PAP; transgenic plant;
resistance; potato virus X; potato virus Y; potato leaf roll virus;
tuber; ss.
Phytolacca americana.
US6015940-A.
18-JAN-2000.
07-APR-1992: 92US-0865169.
07-APR-1992: 92US-0865169.
(MONS) MONSANTO CO.
Kaniowski WK, Tumer NE, Lodge JK:
WPI; 2000-126326/11.
Production of transgenic potato plants or tubers expressing pokeweed
antiviral protein which are resistant to potato virus X or Y -
Claim 7; Fig 5; 30pp: English.
This is the coding sequence for a variant spring leaf form of the
pokeweed antiviral protein (PAP) which is used to generate transgenic
potato plants. PAP is able to confer resistance to infection by potato
virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV)
in the potato plant or tuber expressing PAP. PAP varies from PAP
(AAZ59220) by mutations L20R and Y49H.
Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 other;

Query Match 66.8%; Score 629.2; DB 21; Length 1379;
Best Local Similarity 79.8%; Pred. No. 1.7e-165;
Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
3 GAAGGTCATCTTCTAGTCTGCTGACCTTAATAGCGCTGCTCATCTGCTGACCACTTC 62
221 GAAGATCAAGTCATCTGCTGCTGACCAATATCAATATGCTGCTCATCTGCTGACCACTTC 280
63 AACCTGTGCTCAATAACGATCAGCTTTGATGCTGGAATGCCACCATTAACAAATATGC 122
281 AACCTGTGCTGTAATACATCATCTACATGTTGGAATGCCACCATTAACAAATATGC 340
123 CACCTTTATGAATCTCTGTAATCAAGGAAAGATCCAAATTAATGCTATGCTATGCAT 382
341 CACCTTTGGAATGATCTCTGTAATGAAGGAAAGATCCAAATTAATGCTATGCTATGCAT 400
183 ACCAATGCTACCTGATCTACTTAATTCGACCCCTTAATGCTATGCTATGCTATGCTATGC 242
401 ACCAATGCTGCTCAATACATCAATACAAATGCCACCATTAACAAATATGC 460
243 AACCTTAAACCAATTAATGCTGAGACCAATTAATGCTATGCTATGCTATGCTATGCTATGC 302
461 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 520
303 TGATCCCTTCAATGCGCAATAGTCTGCTTACCATATATTAATGATATTAACAGCACCGA 362
521 TGATCCCTTCAATGCGCAATAGTCTGCTTACCATATATTAATGATATTAACAGCACCGA 580
363 ACACCTGATGCTGCGCAATAGTCTGCTTACCATATATTAATGATATTAACAGCACCGA 422
581 ACACCTGATGCTGCGCAATAGTCTGCTTACCATATATTAATGATATTAACAGCACCGA 640

RESULT 7

AAQ43967

ID: AAQ43967 standard; DNA: 2472 BP.

XX AAQ43967;

AC AAQ43967;

XX 09-NOV-1993 (first entry)

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

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XX Pokeweed antiviral protein.

XX Pokeweed antiviral protein.

cells and purifying the protein from inclusion bodies. The
antiviral proteins and recombinant proteins inhibit protein
synthesis. They can be used as active ingredients of antiviral
agents of plant viruses, and employed in the manufacture of
immunoconjugates for the treatment of AIDS and cancer. The
isolated genes can be used in the breeding of transgenic plants
having viral resistance.

Query Match 62.3%; Score 588.6; DB 19; Length 882;
Best Local Similarity 80.3%; Pred. No. 3e-154;
Matches 703; Conservative 0; Mismatches 169; Indels 3; Gaps 1;

74 TAAATACGATCCTTGGTGGTAAATGCCACCAATTAACAAATATGCCACCTTTATG 133
5 TGAATACCATCTACATCTGTTGGAAGTACCACCATAGCAATAGCCACTTTTCTGG 64
134 ATCTCTTCTGTAATCAAGCAAGATGCCAAATTAATGCTATGCAATACCAATGCTAC 193
65 ATAATCTTGGTAATGAAGCAAGATGCCAAATTAATGCTATGCAATACCAATGCTTC 124
194 CTGATACCTAATCGACCCCTAGTACTTATGTTAAGCTCCAGGTGCAAACTTAA 253
125 CCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 184
254 CCATTAACACTAATGCTGAGCAATCAATCAATCAATCAATCAATCAATCAATCA 313
185 CCATCACTAATGCTGAGCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 244
314 ATGGCAATAGTCTGTTACCATATATTAATGATATTAACAGCAGCCAGCACTGATG 373
245 ATACCAATAGTCTGTTACCATATATTAATGATATTAACAGCAGCCAGCACTGATG 304
374 TGGAGAACTACTCTTCTGCTCAAGTTCTAGTCTGCTGCTGCTGCTGCTGCTGCT 433
305 TAGAGACTACTCTTCTGCTCAAGTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTG 364
434 GCTTATATCCGACCATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 493
365 GTGATATCCACATTTGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTTCACCTG 424
494 GAATCAATATCTCAGCATGACATGGAATAATCTCTGGAGTGTGATTCATTCCTCTAA 553
425 GAATCAATATCTCAGCATGACATGGAATAATCTCTGGAGTGTGATTCATTCCTCTAA 484
554 AAACCTGAGGCTTTTCTTCTACTGAGCCATCAATGCTTCAAGAGGAGCCGATTC 613
485 AGCTGAGCTGAATTCCTCTACTGAGCCATCAATGCTTCAAGAGGAGCCGATTC 544
614 AGTACATAGAGAACCAAGTCAAGACTAATTTAATAGAGCATTCCTGATCCCAAG 673
545 AGTACATAGAGAACCAAGTCAAGACTAATTTAATAGAGCATTCCTGATCCCAAG 604
674 TAATTAATTTGAGGAGAGTGGGCAAAATCTCTCAGGCAATTCACATGCCAAGATG 733
605 TACTTAATTTGAGGAGAGTGGGCAAAATCTCTCAGGCAATTCACATGCCAAGATG 664
734 GGGCTTTTACCCAAACCTTGAAGTGGATGCGCAAGAGTACCAGTGCATGATTCCTTA 793
665 GAGTTTACCCAAACCTTGAAGTGGATGCGCAAGAGTACCAGTGCATGATTCCTTA 724
794 GAGTGGATGAATCAATCTGATGCGCACTCTTAAAGTACCTTAAAGTACCTGTCAGA 853
725 GAGTGGATGAATCAATCTGATGCGCACTCTTAAAGTACCTTAAAGTACCTGTCAGA 784
854 CAACCTT---ACCAAAATGCTGCTCTCAAGTATTAATTTCTACTTATTATTAATA 910
785 CAATTAATCAACCAATGCGCTGTTCTCCTCACTTATATGCTACTTATTATTAATA 844
911 TCTCTAATCTTGGTGTATCTATTGAGCAATTTCTAA 945
845 TGGCTAATCATGCTGATCAGTTTGGGGTCTCTGA 879

RESULT 9
AA199557
ID AA199557 standard; DNA: 2369 BP.
XX
AC AA199557;
XX
DT 08-JUN-1998 (first entry)
XX
DE Phytolacca insularis antiviral protein gpIP50 gene.
XX
KW Antiviral protein; gpIP50 gene; virucide; transgenic plant;
KW virus resistance; immunoconjugate; AIDS; cancer; therapy; ss.
OS Phytolacca insularis Nakai.
XX

Key Location/Qualifiers
CAAT_signal FT 983..986
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TATA_signal FT 1032..1035
/*tag= b
TATA_signal FT 1090..1093
/*tag= c
CDS FT 1128..2075
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sig_peptide FT 1128..1199
/*tag= e
mat_peptide FT 1200..2072
/*tag= f
polyA_signal FT 2142..2146
/*tag= g
polyA_signal FT 2263..2268
/*tag= h
EP808902-A2.
XX
XX 26-NOV-1997.
XX
XX 30-SEP-1996; 96EP-0307159.
XX
XX 22-MAY-1996; 96KR-0017404.
XX (JINK-) JIN RO LTD.
XX
XX Choi J, Choi K, Choi Y, Hong E, Jin J, Kim C;
XX Kim M, Lee J, Lee J, Moon Y, Song S, Yun Y;
XX
XX WPI: 1998-001788/01.
XX P-PSDB: AAW26774.

Antiviral proteins of Phytolacca insularis Nakai and their genes
useful in plant antiviral agents and immunoconjugates for the
treatment of AIDS and cancer
Claim 3: Fig 5; 26pp; English.

This polynucleotide comprises the Phytolacca insularis Nakai gene
coding for a 35.7 kDa novel antiviral protein designated gpIP50
(see AAW26774). The gpIP50 gene was isolated from leaf genomic DNA
using the coding region of antiviral protein cIP as probe.
Another gene (see AA199556), encoding a 32.8 kDa protein (see AAW26774)
designated gpIP2, has also been isolated from P. insularis Nakai.
Also claimed are vectors encoding these antiviral proteins and host
cells transformed or transfected with these vectors. E. coli
XL1-Blue MRF' gpIP50 (MCM-1008) host cells are claimed, as is a
process for preparing antiviral protein by culturing these cells
and purifying the protein from inclusion bodies. The antiviral
proteins and recombinant proteins inhibit protein synthesis. They
can be used as active ingredients of antiviral agents of plant
viruses, and employed in the manufacture of immunoconjugates for
the treatment of AIDS and cancer. The isolated genes can be used

CC in the breeding of transgenic plants having viral resistance.

XX Sequence 2369 BP; 778 A; 373 C; 450 G; 768 T; 0 other;

Query Match 62.1%; Score 586.4; DB 19; Length 2369;
Best Local Similarity 78.9%; Pred. No. 1.8e-153;
Matches 753; Conservative 0; Mismatches 186; Indels 15; Gaps 4;

1 ATGAAGTGCATGCTTCTAGTCTGGTGGTAAATAGCGTGGTCTTCTGTCACCAACT 60
1128 ATCAAGATCATGCTTCTGCTGGTATCAACAATAACAGCATGGCTAATTTTGCACCGCT 1187
61 TCNACTTGTGCC-----ATAAATAGATCACCTTTGTGCTGGAAATGCCACCATTAAC 114
1188 TCAACTTGGCGCCCAAGTCCAAATCAACCTTCGAGTTGGAAATGCGACCATTAAC 1247
115 AAATATGCCACCTTTATGCAATCTCTCGTAAATCAAGCGAAAGATCCAAACCTAAATCC 174
1248 AAGTACGCCACTTTTATGAATCTCTCGTGAATCAAGCGAAAGATCCAAACCTTAATG 1307
175 TATGCGATACCAATGCTACCTGATCTAATTCGACCCCTAACTTATTTGTTAAAGCTC 234
1308 TATGCGATACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1367
235 CRAAGTGCACCACTTAAACCATTAACCTTAATGCTGAGCAAGAAATACCTTATGCTGATG 294
1368 CAAGATTCAGTTTAAACCATTAACCTTAATGCTGAGCAAGAAATACCTTATGCTGATG 1427
295 GGTATTCGATCCCTTCAATGGCAATAGTGTGCTTACCATATATTTAATGATATTAACA 1544
1428 GGTATTCGATCCCTTCAATGGCAATAGTGTGCTTACCATATATTTAATGATATTAACA 1484
355 ---AGCAGCAACGCTGATGCTGAGTAACTCTTTGCTCAAGTTCTAGTTCTCTGCTGTT 411
1485 AATAGTGCATGCAAGTAACTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1544
412 GCAATGCTCAATTAACCTAATAGTGTGCTTACCATATATTTAATGATATTAACA 471
1545 GGTAAATATTAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1601
472 TCAAGAAATCAAGTCCCAATTTGGAAATCAATTAATGCTGAGCAAGTAACTCTCTCT 531
1602 TCAAGAAATCAAGTCCCAATTTGGAAATCAATTAATGCTGAGCAAGTAACTCTCTCT 1661
532 CGAGTTGATTCATTCCTGCTGAAATCAAGTCTTTTCTGCTGCTGCTGCTGCTGCTGCT 591
1662 CGAGTTGATTCATTCCTGCTGAAATCAAGTCTTTTCTGCTGCTGCTGCTGCTGCTGCT 1721
592 GTTTCAGAGCGAGCGGATTCAGTACATAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCA 651
1722 GTTTCAGAGCGAGCGGATTCAGTACATAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCA 1781
652 GCATTCATACCTGATCCCAATTAATTTGGAGGAGGAGTGGGGGCAAAATCTCTGAG 711
1782 GCATTCATACCTGATCCCAATTAATTTGGAGGAGGAGTGGGGGCAAAATCTCTGAG 1841
712 GCAATTCACAAATGCCAAGATGGGCTTTACCCAAACCACTTGTAGCTAGTGGATGCCAA 771
1842 GCAATTCACAAATGCCAAGATGGGCTTTACCCAAACCACTTGTAGCTAGTGGATGCCAA 1901
772 GTTTCAGAGCGAGCGGATTCAGTACATAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCA 831
1902 GTTTCAGAGCGAGCGGATTCAGTACATAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCA 1961
832 TACGTTAATGGAACCTGTGAGCAACTTACCAAAATGCCATGCTTCTCTCAAGTTATAATT 891
1962 TACGTTAATGGAACCTGTGAGCAACTTACCAAAATGCCATGCTTCTCTCAAGTTATAATT 2021
892 TCTACTTATTAATTAATGCTTAACTTCTGATGCTTAACTTCTGATGCTTAACTTCTGAT 945
2022 TCTACTTATTAATTAATGCTTAACTTCTGATGCTTAACTTCTGATGCTTAACTTCTGAT 2075

RESULT 10

ABA96543
ID ABA96543 standard; DNA; 2369 BP.

XX ABA96543;

XX 19-MAR-2002 (first entry)

XX PhytoIaccas insularis antiviral protein (PIP)-encoding DNA.

XX Antiviral protein; PIP; cloning vector; ds.

XX PhytoIaccas insularis.

XX Location/Qualifiers

FT 1128..2075

FT /tag= a

FT /product= "PhytoIaccas insularis antiviral protein, PIP"

FT /tag= b

FT 1200..2072

FT /tag= c

FT /product= "Mature PIP"

XX KH98021298-A.

XX 25-JUN-1998.

XX 16-SEP-1996; 96KR-0040110.

XX 16-SEP-1996; 96KR-0040110.

XX (JINR-) JIN RO LTD.

XX Moon YH, Choi JN, Yoon YC, Jin JH, Hong EJ, Lee JH, Chang JI;

XX Park YC, Choi GH, Kim CH, Kim MG, Song SG, Lee JS, Choi YD;

XX WPI; 1999-299928/25.

XX P-PSDB; AAM53033.

XX Cloning vector using gene of PhytoIaccas insularis antiviral protein

XX (PTP)

XX Example 1; Fig 1; 9pp; Korean.

XX The invention relates to cloning vectors comprising a gene encoding

XX the PhytoIaccas insularis antiviral protein, PIP (ABA96543, AAM53033), or

XX a fragment thereof. The present sequence represents DNA encoding PIP.

XX Sequence 2369 BP; 778 A; 373 C; 450 G; 768 T; 0 other;

XX Query Match 62.1%; Score 586.4; DB 20; Length 2369;

XX Best Local Similarity 78.9%; Pred. No. 1.8e-153;

XX Matches 753; Conservative 0; Mismatches 186; Indels 15; Gaps 4;

QY 1 ATGAAGTGCATGCTTCTAGTCTGGTGGTAAATAGCGTGGTCTTCTGTCACCAACT 60

Db 1128 ATCAAGATCATGCTTCTGCTGGTATCAACAATAACAGCATGGCTAATTTTGCACCGCT 1187

QY 61 TCNACTTGTGCC-----ATAAATAGATCACCTTTGTGCTGGAAATGCCACCATTAAC 114

Db 1188 TCAACTTGGCGCCCAAGTCCAAATCAACCTTCGAGTTGGAAATGCGACCATTAAC 1247

QY 115 AAATATGCCACCTTTATGCAATCTCTCGTAAATCAAGCGAAAGATCCAAACCTAAATCC 174

Db 1248 AAGTACGCCACTTTTATGAATCTCTCGTGAATCAAGCGAAAGATCCAAACCTTAATG 1307

QY 175 TATGCGATACCAATGCTACCTGATCTAATTCGACCCCTAACTTATTTGTTAAAGCTC 234

Db 1308 TATGCGATACCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1367

QY 235 CRAAGTGCACCACTTAAACCATTAACCTTAATGCTGAGCAAGAAATACCTTATGCTGATG 294

1368 CAAGATTCAAGTTTAAAGAACCATCACACTAATGTTGAAGCAAAATCACTGTATGTTATG 1427
295 GGCTATTCTGATCCCTTCAATGGCAATAGTGTCTTACCATATATATTAATGATATACA 354
1428 GGTATGCTGACACCTATAAT---ACAAAGTGTCTGTTATCATATATTTAAGGATATCTCA 1484
355 ---AGCACCGACGACTGATGTGGAGAAATACTCTTTGCTCAAGTCTCTGTTCTGTT 411
1485 AATACTACTGAACAAATGATGTGATGACTACTCTTCTGCTCAAAATATGAGTCTCTGTT 1544
412 GCAATGCTCACTACTACATGATGTTATATCCGACCATGGAAGCAAGCAAGCAAGTAAAC 471
1545 GGTAAATAATATGCTATGATAGCAGTTTCCAGCATTTGGAAGAAAGAGTAGACGA--- 1601
472 TCAAGAAATCAAGTCCCAATTTGGGAATCTCAATACTCAGCAGTGCATTTGGAATAATCTCT 531
1602 TCAAGAAATCAAGTCCCAATTTGGGAATCTCAATACTCAGCAGTGCATTTGGAATAATCTCT 1661
532 GGAGTTGATTCATTTCCCTGTAAAGAACTGAGCGCTTTTCTTACGTGGTAGCCATCAAGT 591
1662 GGAGTGGATACAGTCAATGAGAAACCGAGCGCAATTTCTTCTAGTAGCCATCAAGT 1721
592 GTTTCAGAGGCGAGCGGATTTCAAGTACATACAGAACCAAGTCAAGTCAATTTTAATAGA 651
1722 GTACAGAGGCAACAGATTCAGTACATAGAAATCAGGTGACAGCTAATTTTAATAGG 1781
652 GCATTCTACCTGATCCCAAGTAAATTAATTTGGAGGAAAGTGGGCAAAATCTCTGAG 711
1782 GCATTCTATCTAATGCAAGTAACTAACTTGGAGGAAACATGGGCTAAGTCTTCTACA 1841
712 GCATTTCACATGCGCAAGATGGGCTTTTACCAACCACTTTGAGTGTGATGCGCAAA 771
1842 GCAATTCATGATGTAAGATGGAGCTTTTACCAACCACTTTGAGTGTGATGCGCAAA 1901
772 GGTACCAAGTGGATGTTCTTAGAGTGATGATCAATCTGATGTGGCACTCTTTAAG 831
1902 GGTACTAAGTGGATGTTCTTAGAGTGATGATCAATCAACCTGATGTGGGACTCTTTAAG 1961
832 TACCTTAATGAACCTGTACAGCAACTTACCAAAATGCCATGTTCTCTCAAGTTATAAT 891
1962 TACCTTGAAGGAGCTGTACAGCAACTTACCAAAATGCCATGTTCTCTCAAGTTATAAT 2021
892 TCTACTTATTAATATATCTCTAATCTCTGATCTATTTGAAGGATTTCTAA 945
2022 TCTACTTATTAATATATAGTTAATCTCTGATGATGTTGAGGGTTCTGA 2075

RESULT 11
AA064893
ID AA064893 standard; CDNA; 918 BP.
XX AA064893;
AC AA064893;
XX
DT 17-JAN-1995 (first entry)
XX
DE Antiviral protein of Phytolacca insularis Nakai.
XX
KW Antiviral; anti-microbial; bacteriocide; ribosome; inhibition;
XX inactivation; Phytolacca insularis Nakai; ss.
XX
XX Phytolacca insularis Nakai.
XX
FH Key Location/Qualifiers
FT CDS 1..918
FT /*tag= a
FT /product= Antiviral protein.
XX
XX AU648475-B.
XX
XX 21-APR-1994.
XX
XX 13-OCT-1993: 93AU-0048972.
XX

28-AUG-1993: 93KR-0016938.
(JINR-) JIN RO LTD.
Hong-seob J, Kwan-ho I, Kyu-whan C, Man-keun K;
Young-ho M;
WPI: 1994-167846/21.
P-PSOB: AAR54839.
Nucleotide sequence from Phytolacca insularis encoding antiviral protein - encodes a ribosome inactivating protein which may be used in antimicrobial compsns.
Claim 1: Page 13; 22pp; English.
The antiviral protein encoded by this sequence comprises an amino acid sequence prevalent in ribosome inactivating proteins (see AAR54840). The protein may be used in anti-microbial compositions.
Sequence 918 BP; 294 A; 177 C; 191 G; 256 T; 0 other;

Query Match 57.58; Score 543.8; DB 15; Length 918;
Best Local Similarity 77.48; Pred. No. 141;
Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

Qy 8 TGATGCTTCTAGTGTGCTGACGTTAATAGCGTGGCTCATTTGCTGSCACCACTTCAACTT 67
Db 2 TGAAGTTGATGCTTGTGTCGACATATCAGTATGGCTCATTTGACCAACATCTACTT 63
Qy 68 GTGCCATAAATACGATCACTTGTGATGCTGGAATGCCACCATTAACAAATATGCTACT 127
Db 62 GGGCGGTGAATACGATGCTTACCATGCTGCAAGTACCACCATTAGAAATATATGCAACT 121
Qy 128 TTATGGAATCTCTGCTGAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 187
Db 122 TTGATA---CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 175
Qy 188 TGCTACCTGATCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 176 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
Qy 248 TAAAGCAATCTACACTAATCTGAGACGAAATATATACGATGCTGCTGCTGCTGCTGCT 307
Db 236 AAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 295
Qy 308 CTTTCAATGCAATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
Db 296 CCTACAA---CAATAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
Qy 368 CTGATGTGGAGAACTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
Db 353 AAGATGTAGAGACTACTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412
Qy 428 ACAATAGCTTATATCCGACCATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 487
Db 413 ATGATAGCTGATATCCCAATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 472
Qy 488 AATTGCAATTTCAAAATCTCAGCAGTGCATGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 547
Db 473 AACTGGGAATTCGAATCTCAGCAGTGCATGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 532
Qy 548 CTGTAAAACCTGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
Db 533 CTGAGACAACCGAAGCTGAATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592
Qy 608 GATTCAAGTACATGACCAAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 667
Db 593 GATTCAAGTACATGAGGCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 652
Qy 668 CCAAGTAAATTTGAGGCAAGTGGGCAAGTGGGCAAGTGGGCAAGTGGGCAAGTGGGCAAG 727
Db 653 CCAAGTAAATTTGAGGCAAGTGGGCAAGTGGGCAAGTGGGCAAGTGGGCAAGTGGGCAAG 712

QY 728 AGAATGGGCTTTTACCCAAACCACTTGAGCTAGTGGATGCCAAGATCAACTGGATAG 787
 DB 713 GGAATGGAGCTTTTACCCAAATCCTCTACAGCTAGTGCATGCCAATGGTCCAAATTTGATAG 772
 QY 788 TTCTTAGAGCTGAGTGAATCAATCGTGTGGCTGCGACTCTTAACTACCTTAAATGGCACT 847
 DB 773 TGTGAGAGTGGATGAATCAAGCTTGAATGTCTACTCTTAACTACCTTAAATGGCACT 832
 QY 848 GTCAGACAACTT---ACCAAAATGCCATGCTCTCTCAAGCTTAAATTTCTACTTATATA 904
 DB 833 CCCAGAGAACTTATAACCAAAATGCCAATGTTTCTCAACTTATAATGCTACTTATATA 892
 QY 905 ATTATATGCTTAATCTTGGTGAT 927
 DB 893 ATTACATGCTTAATCTTGGTGAT 915

RESULT 12

AAT04782
 ID AAT04782 standard; DNA: 918 BP.

AC AAT04782;

DT 16-MAY-1996 (first entry)

DE DNA pJMC201 fragment encoding P. insularis antiviral protein.

KW pJMC201; Phytoleuca insularis antiviral protein; PIP; Nakai;

KW primer: amplify; CamV 35S promoter; transgenic plant; potato;

KW Agrobacterium tumefaciens LBA 4004; plant cell transformation; ss.

OS Phytoleuca insularis.

Key Location/Qualifiers

misc_difference 913..915

/tag= a

/codon= seq.gat, aa:Ser

XX AU663031-B.

XX 21-SEP-1995.

XX 04-OCT-1994; 94AU-0074404.

XX 21-JUL-1994; 94KR-0017696.

XX (JINR-) JIN RO LTD.

XX Chul-Hwan K, Hong-Seob J, Kyu-Whan C, Man-Keun K;

PI Young-Ho M;

XX WPI; 1995-358858/47.

XX P-PSDB; AAR80106.

PT Recombinant DNA vector expressing Phytoleuca insularis antiviral

PT protein - for the production of virus resistant transgenic plants

PS Example 1; Fig 1; 25pp; English.

XX This sequence represents a fragment of a recombinant DNA pJMC201 and
 CC encodes Phytoleuca insularis antiviral protein (PIP). This sequence
 CC was isolated from a cDNA library of Phytoleuca insularis Nakai using
 CC the primer sequences given in AAT04782-84. The amplified sequence was
 CC used, cloned with the CamV 35S promoter, in the production of a
 CC transgenic plant, pref. potato, using Agrobacterium tumefaciens LBA
 CC 4004 for plant cell transformation.

XX Sequence 918 BP; 294 A; 177 C; 191 G; 256 T; 0 other;

XX Query Match 57.5%; Score 543.8; DB 16; Length 918;

XX Best Local Similarity 77.4%; Pred. No. 1e-141;

XX Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

QY 8 TCATGCTTGTACTTGTGGTGCACCTTAATAGCTGGCTCATTCCTGCACCAACTTCAACTT 67
 DB 2 TCAGTGTGATGCTTGTGGTGCACAAATATACATGCTATGCTCATCTTCTGCACCAACTTCAACTT 63
 QY 68 GTGCCATAATACGATCAGCTTGTGATGCTGGGAAATGCCACCATTAACAATAATACCACTT 127
 DB 62 GGGCTGCTCAATACCATCTTACCATCTGCTGCAAGTACCACTTACCAACTTACCAACTT 121
 QY 128 TTATGCAATCTCTTGTGTAATCAAGCAAGATGCCAAGCTTAAATGCTATGCTATATCA 187
 DB 122 TTGGATA---CTTGTGTAAGGCAAGATGCT---AAGTTATGCTATGCTATGCTATGCTAT 175
 QY 188 TGCTACCTGATCTAATTCGACCCCTTAAGTACTTATTTGCTTAAGCTTCCAAAGTGCACAC 247
 DB 176 TGCTGCCCAATATTTGATCAAAATCCAAATACATATTTGCTTCCAGCTTCCAAAGTGCAC 235
 QY 248 TAAACCACTTACACTAATGCTGAGACGAAATAACTTATACCTGATGGGCTATTTCTATC 307
 DB 236 AAGAAGGCTACACTAATGCTAAGCAAGCAAAATTTATATGCTGATGGGCTATTTCTATC 295
 QY 308 CCTTCAATGCAATAGTCTGCTTACCATATATTTAATCATATTTAATCATATTTAATCAT 367
 DB 296 CCTACAA---CAATAGTGTGCTTCCATCTCTTTAAGGCTATCTCAGGTACTGCAAGCTG 352
 QY 368 CTGATGCTGGAGAACTACTTCTGCTCAAGTCTTAGTCTCTGCTGTTGCAATGCTCATTA 427
 DB 353 AAGATGTACAGACTACTCTTTGCCCAATGCGGATTCGCTGCTGGTAAACATAAATCT 412
 QY 428 ACAATAGCTTATATCGGACCATGGAAGCAAGACAGAGTAACTCAAGAAATCAAGTCC 487
 DB 413 ATGATAGTGCATATCCAACTTGAATCAAAAGCAGGAGTAAATTCAGAAATTCAGTCC 472
 QY 488 AATTGGGAATTCAAATACTCAGCAGTGCATTTGGAATAATCTCTGAGTTGATTCATTC 547
 DB 473 AACTGGAATTCGATACCTGACAGCTGGCATTTGGAGGATTTCTGGAGTGCATTCATTC 532
 QY 548 CTGTAAAACTGAGGCTTTTTTTTCTACTGGTAGCTCCAAATGTTTTCAGAGGAGGCTC 607
 DB 533 CTGAGAGAACCGAAGCTGAATTCCTACTGCTAGCCATACAAATGCTATCAGAGGAGTAA 592
 QY 608 GATTCAAGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGAGCATCTTCTATCTGAT 667
 DB 593 GATTCAAGTACATAGAGGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 652
 QY 668 CCAAGTAAATTAATTTGGAGGAGAGTGGGCAAAATCTCTCAGGCAATTCACAAATGCCA 727
 DB 653 CCNAAGTACTTATATTTGAGGAGACATGCGGTAAAGATTTCTTCACCAATTCATGCTG 712
 QY 728 AGAATGGGCTTTTACCCAAACCACTTGAAGTGGATGCCAAGGTACCAAGTGCATAG 787
 DB 713 GGAATGGAGTTTTACCCCAATCTCTACAGCTAGTGCATGCCAATGGTGCATAATTCGAT 772
 QY 788 TTCTTAGAGTGGATGAATCAATCTGATGCTGGCACTCTTAACTACCTTAACTGCAACT 847
 DB 773 TGTGAGAGTGGATGAATCAAGCTGATGCTGCTCTCTCAAGTATTAATTTCTACTTATATA 832
 QY 848 GTCAGACAACTT---ACCAAAATGCCATGCTTCTCTCAAGTATTAATTTCTACTTATATA 904
 DB 833 GCCAGAGAACTTATAACCAAAATGCCATGTTTCTCAACTTATAATGCTACTTATATA 892
 QY 905 ATTATATGCTTAATCTTGGTGAT 927
 DB 893 ATTACATGCTTAATCTTGGTGAT 915

RESULT 13

AZ45198

ID AZ45198 standard; DNA: 934 BP.

XX AZ45198;

DT 29-FEB-2000 (first entry)

09978274

SRNT

Printed 11/17/2004

06/02/2003

Db 59 IPMLPNTNPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 118
Qy 121 ERTDVENTLCSSSSRVAMSYNINSLYPTMEKKAENSRNOVOLGQIOLSSDGTGKISGVD 180
Ub 119 ERQDVETTLCPNANSRVSKINFDSPRTLESKAGVSRSOVOLGQIOLSSDGTGKISGVD 178
Qy 181 SPVPKTEAFFLLVAIOHVSAAAFKTYENOVKTNFNAFYDPKVINLEEKWKCKISPAH 240
Db 179 SFTEKTEAEFFLLVAIOHVSAAAFKTYENOVKTNFNAFYDPKVINLEEKWKCKISPAH 238
Qy 241 NAKKCALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTY-QHAFESQVLIIST 299
Db 239 DAKNGVLPKPLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTY-QHAFESQVLIIST 298
Qy 300 YNYMNLGOLFEGF 314
Db 299 YNYMNLGOLFEGF 313

RESULT 2
S28421
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed
N:Alternate names: antiviral protein alpha-PAP
C:Species: Phytolacca americana (Virginian pokeweed)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C:Accession: S28421
R:Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.
Plant Mol. Biol. 20, 879-886, 1992
A:Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein
A:Reference number: S28421; MUID:9309240; PMID:1281438
A:Accession: S28421
A:Molecule type: DNA
A:Residues: 1-294 <RNG>
A:Cross-references: EMBL:D10600; NID:g218010; PIDN:RAA01451.1; PID:g218011
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase
F:30-278/domain: rRNA N-glycosidase homology <RNG>

Query Match 68.9%; Score 1113.5; DB 2; Length 294;
Best Local Similarity 75.4%; Pred. No. 3.9e-78;
Matches 221; Conservative 27; Mismatches 42; Indels 3; Gaps 3;

Qy 1 MKVMLVVVVVTLIANLIAPSTCAINITFDAGNATINKYATFMSLRNOAKDPKLCYCG 60
Db 1 MKMVMVVVMMLSLILKPPSTWAINITFDVGNATINKYATFMSLRNOAKDPKLCYCG 60
Qy 61 IPMLPNTNPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 119
Db 61 IPMLPNTNPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 119
Qy 120 TERTDVENTLCSSSSRVAMSYNINSLYPTMEKKAENSRNOVOLGQIOLSSDGTGKISG 179
Db 120 TERTDVENTLCSSSSRVAMSYNINSLYPTMEKKAENSRNOVOLGQIOLSSDGTGKISG 178
Qy 180 DSFPVKTEAFFLLVAIOHVSAAAFKTYENOVKTNFNAFYDPKVINLEEKWKCKISPAH 239
Db 179 DSFPVKTEAFFLLVAIOHVSAAAFKTYENOVKTNFNAFYDPKVINLEEKWKCKISPAH 238
Qy 240 HNAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTY-QHAFESQVLIIST 299
Db 239 HNAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTY-QHAFESQVLIIST 298

RESULT 3
JE0401
antiviral protein - Virginian pokeweed
C:Species: Phytolacca americana (Virginian pokeweed)
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 07-May-1999
C:Accession: JE0401
R:Kung, S.S.; Kimura, M.; Funatsu, G.
Agric. Biol. Chem. 54, 3301-3318, 1990
A:Title: The complete amino acid sequence of antiviral protein from the seeds of pokeweed
A:Reference number: JE0401; MUID:91242096; PMID:1368643

A:Accession: JE0401
A:Molecule type: protein
A:Residues: 1-261 <KUN>
A:Experimental source: seed
C:Comment: This protein prevents the replication of a number of plant viruses, and
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:6-254/Domain: rRNA N-glycosidase; glycoprotein
F:10,44,255/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:34-258,84-105/Disulfide bonds: #status experimental

Query Match 67.8%; Score 1096.5; DB 2; Length 261;
Best Local Similarity 82.0%; Pred. No. 6.7e-77;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

Qy 25 INITFDAGNATINKYATFMSLRNOAKDPKLCYCG1PMLPNTNPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 286
Db 1 INITFDAGNATINKYATFMSLRNOAKDPKLCYCG1PMLPNTNPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 261

Qy 85 TITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 286
Db 61 TITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 261

Qy 145 SLPTTEKKAENSRNOVOLGQIOLSSDGTGKISGVSFPVKTEAFFLLVAIOHVSAAAF 204
Db 120 GLYPTLEKKAENSRNOVOLGQIOLSSDGTGKISGVSFPVKTEAFFLLVAIOHVSAAAF 179

Qy 205 KYTENOVKTNFNAFYDPKVINLEEKWKCKISPAHNAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTY 286
Db 180 KYTENOVKTNFNAFYDPKVINLEEKWKCKISPAHNAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTY 261

Qy 265 RVDEINRDVALLKYVNGTCOTTY 286
Db 240 RVDEINRDVALLKYVNGTCOTTY 261

RESULT 4
S46239
ribosome-inactivating proteins - Virginian pokeweed
C:Species: Phytolacca americana (Virginian pokeweed)
C:Date: 10-Dec-1994 #sequence_revision 12-May-1995 #text_change 20-May-1999
C:Accession: S46239
R:Boyer, J.L.; Radom, J.; Hoeveler, A.
FEBS Lett. 347, 268-272, 1994
A:Title: Isolation and characterization of a cDNA clone encoding the pokeweed anti-viral
A:Reference number: S46239; MUID:94307398; PMID:8034016
A:Accession: S46239
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-310 <POY>
A:Cross-references: GB:X78028; NID:g517180; PIDN:CAA55342.1; PID:g517181
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:29-282/Domain: rRNA N-glycosidase homology <RNG>

Query Match 31.6%; Score 511; DB 2; Length 310;
Best Local Similarity 39.9%; Pred. No. 7.8e-32;
Matches 130; Conservative 53; Mismatches 111; Indels 12; Gaps 14;

Qy 1 MKVMLVVVVVTLIANLIAPSTCAINITFDAGNATINKYATFMSLRNOAKDPKLCYCG 60
Db 3 MKVLEVVVGLAISLMLTTP---ASSNIVFVENATPETYSNFLTSLEAVKDKKLTCHG 59

Qy 61 IPMLPNTNPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 299
Db 60 MINATVTLTEQPKYVLCVLOGLSNKKTITLMLRNNLYVMGYSDPFTNKRHYHIFNDISGT 113

Qy 121 ERTDVENTLCSSSSRVAMSYNINSLYPTMEKKAENSRNOVOLGQIOLSSDGTGKISG 178
Db 114 SESDAQETVCPGKSPGTONNIPYKSKYKMSKSG---GARTLGLGKIKITLKSNNKIVG 171

Qy 179 VDSPP-----VKTEAFFLLVAIOHVSAAAFKTYENOVKTNFNAFYDPKVINLEEKWKCKISPAH 232
Db 172 KOATDQKQOKNEAEFFLLVAIOHVSAAAFKTYENOVKTNFNAFYDPKVINLEEKWKCKISPAH 231

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QY   233 GKISEAIHNKNG-----ALPAPLELVDAOKTKWTLVLRVDENRDV-ALLKYVNGTCQT 286
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   232 DVSYSKI--AKVGTSGDSTVTLPGLDKDENKNKPMTTATMDNLKNDIMALLTHV--TKCV- 286
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY   287 YONAFESOVIIISTYYNMSNLGDLFE 312
      :|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB   287 -KSSMPPEI MSYYRTSISLUGE-FE 310
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
T12573
rRNA N-glycosidase (EC 3.2.2.22) - common ice plant
N:Alternate names: ribosome-inactivating protein
C:Species: Mesembryanthemum crystallinum (common ice plant)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: T12573
R:Ripmann, J.F.; Michalowski, C.B.; Nelson, D.E.; Bohnert, H.J.
Plant Mol Biol 35, 701-709, 1997
A>Title: Induction of a ribosome-inactivating protein upon environmental sl
A:Reference number: Z17533; MUID:98087998; PMID:942592
A:Accession: T12573
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-289 <RP>
A:Cross-references: EMBL:U080072; NID:g1773331; PIDN:AAB96824.1; PIR:g177333
C:Genetics:
A:Gene: RIP
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase

```

F. 28-271/Domain: rRNA N-glycosidase homologues <BN/1>

Query Match 25.1%; Score 406; DR 2; Length 272;
Best Local Similarity 38.8%; Pred. NO. 7.7e-24;
Matches 111; Conservative 40; Mismatches 113; Indels

[illegible]

F:30-273/Domain: rRNA N-glycosidase homology <RNG>

Query Match 23.4% Score 378.5 DB 2 Length 283;
Best Local Similarity 36.4% Pred. No. 1e-21;
Matches 104; Conservative 56; Mismatches 103; Indels 23; Gaps 10;

Qy 4 MLVVVTLIAWLI---AAPTSTCAINTITDAGNATINKYATFMSLRNNAKDPKLCYC 60
Db 1 MKIYVATIAWILLOFSAWTTDAVTSITLDLYNPTAGVSSFYVDKIRNNVKDPNLKYGG 60
Qy 61 LPM-LPOTNSTPKYLLVLOGANLKTITLMLRRNNLYVMGYSDPFNGKCR-YHIFNDIT 118
Db 61 TDIAVIGPPSKKFLRNFQSSR-GTVSLGLKRONLYVVAWLAMDTNVRAYYFKSEIT 119
Qy 119 STERTDVENTLCSRSSRVAMSYNSLYPTMEKAEV---NSRNOVOLGIGIOLLSSTME 174
Db 120 SAEST-----ALFPEATNOKALEYTEDYOSIEKNAQITOGDQSRKELGIGIOLLSSTME 175
Qy 175 KISGVDSFPVKTEAFFLLVAIQMVSEAAKRYENOVKTNFNRAFYDDPKVINLEEKWGK 234
Db 176 AVN-KKARVVKDEARFLLIAIQMTAEAFRYIQNLVTKNFPNKFSENKVIQFEVNNKK 234
Qy 235 ISEAIH-NAKNGALPKPLELVDAKGTWKWILRVDEINRDVALLKYV-279
Db 235 ISTAIYGDARKGVNKDYDFGFK-----VRQVKDL--QMGLLMYL 273

RESULT 8

RLOH2

rRNA N-glycosidase (EC 3.2.2.22) Sap2 precursor - common soapwort
N:Alternate names: ribosome-inactivating protein; saporin 2; saporin S5
C:Species: Sapontaria officinalis (common soapwort)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jul-1999
C:Accession: S17933; S28540; S38526; S15459
R:Fordham-Skelton, A. P.; Taylor, P. N.; Hartley, M. R.; Croy, R. R. D.
Mol. Gen. Genet. 229, 460-466, 1991
A:Title: Characterisation of saporin genes: in vitro expression and ribosome inactivating
A:Reference number: S17932; MUID:92049247; PMID:1719367
A:Accession: S17933
A:Molecule type: DNA
A:Residues: 1-292 <FOR>
A:Cross-references: EMBL:X59255; GB:S63902; NID:g2094853; PIDN:CAA41948.1; PID:g21321
R:Soria, M. R.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S28540
A:Accession: S28540
A:Molecule type: DNA
A:Residues: 25-283 <SOR>
A:Cross-references: EMBL:X69132; NID:g21330; PIDN:CAA48886.1; PID:g938284
R:Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Rojo,
Biochim. Biophys. Acta 1216, 31-42, 1993
A:Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA
A:Reference number: S38521; MUID:94032486; PMID:8218413
A:Accession: S38526
A:Molecule type: protein
A:Residues: 25-54 <PER>
C:Genetics:

Query Match 23.04% Score 372; DB 1; Length 292;
Best Local Similarity 35.4% Pred. No. 3.4e-21;
Matches 108; Conservative 52; Mismatches 107; Indels 36; Gaps 12;
Qy 4 MLVVVTLIAWLI---AAPTSTCAINTITDAGNATINKYATFMSLRNNAKDPKLCYC 60
Db 1 MKIYVATIAWILLOFSAWTTDAVTSITLDLYNPTAGVSSFYVDKIRNNVKDPNLKYGG 60
Qy 61 LPM-LPOTNSTPKYLLVLOGANLKTITLMLRRNNLYVMGYSDPFNGKCR-YHIFNDIT 118

Query Match 23.04% Score 372; DB 1; Length 292;
Best Local Similarity 35.4% Pred. No. 3.4e-21;
Matches 108; Conservative 52; Mismatches 107; Indels 36; Gaps 12;
Qy 4 MLVVVTLIAWLI---AAPTSTCAINTITDAGNATINKYATFMSLRNNAKDPKLCYC 60
Db 1 MKIYVATIAWILLOFSAWTTDAVTSITLDLYNPTAGVSSFYVDKIRNNVKDPNLKYGG 60
Qy 61 LPM-LPOTNSTPKYLLVLOGANLKTITLMLRRNNLYVMGYSDPFNGKCR-YHIFNDIT 118

Db 61 TDIAVIGPPSKKFLRNFQSSR-GTVSLGLKRONLYVVAWLAMDTNVRAYYFKSEIT 119
Qy 119 STERTDVENTLCSRSSRVAMSYNSLYPTMEKAEV---NSRNOVOLGIGIOLLSSTME 171
Db 120 SAEST-----ALFPEATNOKALEYTEDYOSIEKNAQITOGDQSRKELGIGIOLLSSTME 175
Qy 172 DICKISGVDSFPVKTEAFFLLVAIQMVSEAAKRYENOVKTNFNRAFYDDPKVINLEEK 231
Db 176 AVNKKARV---VKNEARFLLIAIQMTAEAFRYIQNLVTKNFPNKFSDSNKVIQFEVS 231
Qy 232 WKISRAIH-NAKNGALPKPLELVDAKGTWKWILRVDEINRDVALLKYV-----NC 281
Db 232 WRKISTAIYGDARKGVNKDYDFGFK-----VRQVKDL--QMGLLMYLCKPKSSNKANS 284
Qy 282 TCOTT 286
Db 285 TAYAT 289

RESULT 9

S17519

rRNA N-glycosidase (EC 3.2.2.22) dianthin 30 precursor - clove pink
N:Alternate names: DAP30 protein; ribosome-inactivating protein dianthin 30
C:Species: Dianthus caryophyllus (clove pink)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 33-Sep-1998
C:Accession: S17519; S17685
R:Legname, G.; Bellosta, P.; Gromo, G.; Modena, D.; Keen, J. N.; Kokoris, L. M.; Lord,
Biochim. Biophys. Acta 1090, 119-122, 1991
A:Title: Nucleotide sequence of cDNA coding for dianthin 30, a ribosome inactivating
A:Reference number: S17519; MUID:91355219; PMID:1840496
A:Accession: S17519
A:Molecule type: mRNA
A:Residues: 1-293 <LEG>
A:Cross-references: EMBL:X59260
A:Experimental source: Leaf
R:Lee-Huang, S.; Kung, H.; Huang, P. L.; Huang, P. L.; Li, B. Q.; Huang, P.; Huang, H. J.
FEBS Lett. 291, 139-144, 1991
A:Title: A new class of anti-HIV agents: GAP31, DAPS 30 and 32.
A:Reference number: S17574; MUID:92037998; PMID:1936243
A:Accession: S17685

A:Molecule type: protein
A:Residues: 24-40, X, 42-82 <DAP>
C:Genetics:
A:Gene: dia 30
C:Function:
A:Note: high antiviral potency, but low toxicity to cells in culture or intact anima
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: antiviral; glycosidase; hydrolase; monomer; toxin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-293/Product: rRNA N-glycosidase dianthin 30 #status experimental <MAT>
F:29-273/Domain: rRNA N-glycosidase homology <RNG>

Query Match 21.4% Score 345.5; DB 2; Length 293;
Best Local Similarity 34.6% Pred. No. 3.7e-19;
Matches 100; Conservative 52; Mismatches 108; Indels 29; Gaps 12;

Qy 4 MLVVVTLIAWLIAPTS---TCAINTITDAGNATINKYATFMSLRNNAKDPKLCYC- 60
Db 1 MKIYVATIAWILFQSSWTTDAATAYTLNANPSSASQYSSFLDQIRNNVDTSL-IYGG 59
Qy 61 --IPMLPDTNSTPKYLLVLOGANLKTITLMLRRNNLYVMGYSDPFNGKCR-YHIFNDI 117
Db 60 TDVAVIGAPSTTDKFLRNFUGPK-GTVSLGLKRONLYVVAWLAMDTNVRAYYFKNOJ 118
Qy 118 TSTERTDVENTLCSRSSRVAMSYNSLYPTMEKAEV---NSRNOVOLGIGIOLLSSTME 171
Db 119 TSAETITLFPVAVANOKO-----LEYGEDYQALTEKNAKITTDQSRKELGIGIOLLSSTME 171
Qy 174 GKISGVDS--FPVKTEAFFLLVAIQMVSEAAKRYENOVKTNFNRAFYDDPKVINLEEK 231
Db 172 TMDUGVNNKVVYKDEAKFLLIAIUMTAAARFYIQNLVTKNFPNKFSENKVIQFEVS 231

C:Keywords: glycosidase; hydrolase; toxin
F:6-249/Domain: rRNA N-glycosidase homology <RNG>

Query Match 20.98; Score 336; DB 2; Length 253;
Best Local Similarity 35.54; Pred. No. 1.7e-18;
Matches 93; Conservative 51; Mismatches 98; Indels 20; Gaps 9;

QY 25 INTITDAGNATINKYATFMESLRNOAKDPKLCYGYPM-LPDTNSTPKYLLVKOGANL 83
DB 1 VTSITDLVNPTAGQYSSFDKIRNNVKNPKLYGGTDIAVIGPPSKKFLRINFQSSK 59
QY 84 KTTLMRLRNLYVMGYSDPFNGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSIN 142
DB 60 GTVSLGLKRDNLVYVAYLAMDNTNVRAYFRSEITSAELT---ALFPEATANQKALE 115
QY 143 YNSLYPTMEKAEV-----NSRNOVOLGIQILSSDIGIKSGVDFPVKTEAFFLLVAITOMV 198
DB 116 YTEDYOSIENNAQITQDCKSKKELGLDILLTSMKAVN-KKARVVKNKARFLLIATQMT 174
QY 199 SEARFYKIENOVKTENAFYDPKVINLEEKWKITSEATH-NAKNGALPKPLELYDAK 257
DB 175 AEARFYQIQLVKNPNFNSKNKVIQFVNNKKISTALYGOAKNGVKNKYDIPGFGK 234
QY 258 GTRKIVLRVDEINRDVALLKYV 279
DB 235 -----VRQVKDL--QMGLLHYL 249

RESULT 14

S28541
rRNA N-glycosidase (EC 3.2.2.22) (clone G-4) - common soapwort (fragment)
N:Alternate names: ribosome-inactivating protein; saporin
C:Species: Saponaria officinalis (common soapwort)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Aug-1999
C:Accession: S28541
R:Sorta, M.R.

submitted to the EMBL Data Library, October 1992

A:Reference number: S28539
A:Accession: S28541
A:Molecule type: DNA
A:Residues: 1-253 <SOR>
A:Cross-references: EMBL:X69133; NID:Q21331; PIDN:CA448807.1; PID:Q21332
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase; toxin
F:6-249/Domain: rRNA N-glycosidase homology <RNG>

Query Match 20.78; Score 335; DB 2; Length 253;
Best Local Similarity 35.98; Pred. No. 2e-18;
Matches 95; Conservative 47; Mismatches 97; Indels 26; Gaps 10;

QY 25 INTITDAGNATINKYATFMESLRNOAKDPKLCYGYPM-LPDTNSTPKYLLVKOGANL 83
DB 1 VTSITDLVNPTAGQYSSFDKIRNNVKNPKLYGGTDIAVIGPPSKKFLRINFQSSR 59
QY 84 KTTLMRLRNLYVMGYSDPFNGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSIN 142
DB 60 GTVSLGLKRDNLVYVAYLAMDNTNVRAYFRSEITSAELT---ALFPEATANQKALE 115
QY 143 YNSLYPTMEKAEV-----NSRNOVOLGIQIL---SSDIGISGVDSFPVKTEAFFLLVAI 195
DB 116 YTEDYOSIENNAQITQDCKSKKELGLDILLTSMKAVN-KKARV---VKNKARFLLIAT 171
QY 196 QMVSEARFYKIENOVKTENAFYDPKVINLEEKWKITSEATH-NAKNGALPKPLELY 254
DB 172 QMTAEARFYQIQLVKNPNFNSKNKVIQFVNNKKISTALYGOAKNGVKNKYDIPG 231
QY 255 DAKGTRKIVLRVDEINRDVALLKYV 279
DB 232 FGK-----VRQVKDL--QMGLLHYL 249

RESULT 15

JT0753

rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum
N:Alternate names: gelonin; type I ribosome-inactivating protein
C:Species: Gelonium multiflorum
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Aug-1999
C:Accession: JT0753; S16489
R:Nolan, P.A.; Garrison, D.A.; Better, M.
Gene 134, 223-227, 1993
A:Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating
A:Reference number: JT0753; MUID:94085781; PMID:7916721
A:Accession: JT0753
A:Molecule type: mRNA
A:Residues: 1-316 <NOL>
A:Cross-references: GB:L12243; NID:Q388633; PIDN:AAA16312.1; PID:Q388634
R:Montecuchi, P.C.; Lezzarini, A.M.; Barbieri, L.; Stirpe, F.; Sorio, M.; Lippi,
Int. J. Pept. Protein Res. 33, 263-267, 1989
A:Title: N-terminal sequence of some ribosome-inactivating proteins.
A:Reference number: S16331; MUID:89326691; PMID:2753596
A:Accession: S16489
A:Molecule type: protein
A:Residues: 47-89, 'K', 91-92, 'D' <MON>
C:Function:

A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRN
A:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: glycosidase; hydrolase
F:1-46/Domain: signal sequence #status predicted <SIG>
F:47-316/Product: ribosomal RNA N-glycosidase #status predicted <MAT>
F:53-294/Domain: rRNA N-glycosidase homology <RNG>

Query Match 20.48; Score 330; DB 2; Length 316;
Best Local Similarity 30.84; Pred. No. 6.4e-18;
Matches 97; Conservative 60; Mismatches 122; Indels 36; Gaps 11;

QY 7 VVVTLIAWLIAPTS-----TCATNTITFDACNATINKYATFMESLRNOAKDPKLCY 59
DB 23 IVIGSTARIFFSLPTNDEETSKTIGDVTFSFTKGTATJTYVNFLEIRVKLK-PEGNSH 81
QY 60 GIPMLPDTNSTPK--YLLVKLQGANLKITLMLRRNLYVMGYSDPFNGKCRHYLFNDI 117
DB 82 GIPLLRKKCDPCPKCFVLVALSNDNGOLAEITADVTSVYVGYO-----VNRKSYFFKDA 136
QY 118 TSTERTDV-ENTLCSSSSRVAMSINYSLYPTMEKAEVNSRNOVOLGIQILSSDIGIKT 176
DB 137 PDAAEGLFKNT-----IKTRLHFGGSYPSLE--GEKAYRETTDLGTEPLRIGIKKL 186
QY 177 --SGVDSFPVKTEAFFLLVAITOMVSEARFYKIENOVKTENAFYDPKVINLEEKWK 234
DB 187 DENAIDNYKPTETIASLLVVIOMVSEARFTFTENQIRNNFQOIRPANNITISLENKWK 246
QY 235 ISEAIH-NAKNGALPKPLELYDAKTKWIVLRVDEINROVALLKYVNGTCQTTYNAMES 293
DB 247 LSFQIKTSGANCMFSEAVELERANGKYYVTVADQVKNPKIALLLKFDVKDKPT----SLAA 302
QY 294 QVLIISTYNNYMSNLG 308
DB 303 ELTIQ-----NYESLVG 314

Search completed: May 28, 2003, 09:59:04
Job time : 47 secs

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OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 02:32:48 ; Search time 2636 seconds
(without alignments)
10433.290 Million cell updates/sec

US-09-978-274A-1

Title:
Perfect score: 945

Sequence: 1 atgaagtgatgttgtagt.....atctattgaagattctaa 945

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.:

- 1: gb_ba.:
- 2: gb_htg.:
- 3: gb_in.:
- 4: gb_om.:
- 5: gb_ov.:
- 6: gb_pat.:
- 7: gb_ph.:
- 8: gb_pl.:
- 9: gb_pr.:
- 10: gb_ro.:
- 11: gb_sts.:
- 12: gb_sy.:
- 13: gb_un.:
- 14: gb_vl.:
- 15: em_ba.:
- 16: em_fun.:
- 17: em_hum.:
- 18: em_in.:
- 19: em_mu.:
- 20: em_om.:
- 21: em_or.:
- 22: em_ov.:
- 23: em_pat.:
- 24: em_ph.:
- 25: em_pl.:
- 26: em_ro.:
- 27: em_sts.:
- 28: em_un.:
- 29: em_vl.:
- 30: em_htg_hum.:
- 31: em_htg_inv.:
- 32: em_htg_other.:
- 33: em_htg_mus.:
- 34: em_htg_pln.:
- 35: em_htg_rod.:
- 36: em_htg_mam.:
- 37: em_htg_vrt.:
- 38: em_sy.:
- 39: em_htgo_hum.:
- 40: em_htgo_mus.:
- 41: em_htgo_other.:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	6	AX427702 Sequence
2	841	89.0	1249	8	PAPAPSRIP
3	737	78.0	792	6	AX427704 Sequence
4	712	75.3	1092	6	AX427720 Sequence
5	494	52.3	786	8	AB071855 Phytolacc
6	459	48.6	465	6	AX427706 Sequence
7	329	34.8	333	6	AX427708 Sequence
8	42	4.4	42	6	AX427716 Sequence
9	42	4.4	42	6	AX427717 Sequence
10	42	4.4	783	8	AB071854 Phytolacc
11	32	3.4	2472	6	E05033 DNA cinnadi
12	32	3.4	2472	8	PTCAPAP
13	30	3.2	52	6	AX427714 Sequence
14	30	3.2	1164	8	AY049785 Phytolacc
15	29	3.1	1164	8	PAPAP
16	29	3.1	1195	6	A36639 Sequence 1
17	29	3.1	1195	6	A42103 Sequence 1
18	29	3.1	1195	6	T43835 Sequence 1
19	29	3.1	1195	6	155866 Sequence 1
20	29	3.1	1378	6	AX427732 Sequence
21	29	3.1	1379	6	AR009535 Sequence
22	29	3.1	1379	6	AR136704 Sequence
23	29	3.1	1379	6	AR136705 Sequence
24	29	3.1	1379	6	AX427731 Sequence
25	25	2.5	43	6	AX427710 Sequence
26	27	2.9	47	6	AX427713 Sequence
27	27	2.9	49	6	AX427715 Sequence
28	26	2.8	48	6	AX427712 Sequence
29	25	2.6	45	6	AX427721 Sequence
30	24	2.5	43	6	AX427710 Sequence
31	24	2.5	43	6	AX427711 Sequence
32	24	2.5	1387	8	AF445416 Houda Inv 1
33	23	2.4	882	6	A67183 Sequence 1
34	23	2.4	34578	9	AC107069 Homo Sapi
35	23	2.4	46778	2	AC079784
36	23	2.4	187071	2	AC099611
37	22	2.3	918	6	A43003
38	22	2.3	918	6	A48150 Sequence 1
39	22	2.3	918	6	T60482 Sequence 1
40	22	2.3	918	6	T89987 Sequence 1
41	22	2.3	951	6	A67185 Sequence 3
42	22	2.3	2369	8	AF141331 Phytolacc
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45	21	2.2	188647	2	AL772395

ALIGNMENTS

RESULT 1	AX427702	AX427702	945 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427702	Sequence 1 from Patent W00233107.				
DEFINITION	AX427702					
ACCESSION	AX427702					
VERSION	AX427702.1	GI:21537815				
KEYWORDS						
SOURCE		Virginian pokeweed.				
ORGANISM		Phytolacca americana				
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotids;				
		Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE						
AUTHORS		Neelam, A.; Atkinson, H. J.; McPherson, M. J. and Thomas, L. J. R.				
TITLE		Plant cell death system				

JOURNAL Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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/db_xref="taxon:3527"
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variation 750..759
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misc_feature complement(922..945)
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Best Local Similarity 100.0%; Pred No. 0;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TCACTTGTGCCATAAATACGATCACCTTTGATGCTGGAATGCCACCATTAACAATAT 120
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QY 121 GCCACCTTTATGGAATCTCTTCTGTAATCAAGCAAGATCCAAACTAAATGCTATGGC 180
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QY 181 ATACAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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QY 241 GCAACCTTAAACCAATACACTAATGCTGAGAGCAATACCTATATGATGATGATGATGAT 300
Db 241 GCAACCTTAAACCAATACACTAATGCTGAGAGCAATACCTATATGATGATGATGATGAT 300
QY 301 TCTGATCCTTCAATGGAATGCTGCTTACCATATATTAATGATATTTACAGCACC 360
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Db 721 AATGCCAAGATGGGCTTTTACCCAAACCACTTGGAGTGGAGTGGAGTGGAGTGGAGTGG 780
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QY 901 TATAATATATGCTAATCTTGTGATCTATTTGAAGGATCTTAA 945
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RESULT 2
PAPAPSRIP 1249 bp mRNA linear PLN 30-APR-1997
LOCUS P.americana mRNA for pokeweed antiviral protein.
DEFINITION X98079
ACCESSION X98079
VERSION X98079.1 GI:1707648
KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.
SOURCE Phytolacca americana.
ORGANISM Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 1249)
AUTHORS Poyet,J.L. and Hoeweler,A.
TITLE cDNA cloning and expression of pokeweed antiviral protein from seeds in Escherichia coli and its inhibition of protein synthesis in vitro
JOURNAL FEBS Lett. 406 (1-2), 97-100 (1997)
MEDLINE 97263479
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet,J.L.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-1996) J. L. Poyet, Laboratoire de Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Resancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
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1235
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SOURCE
ORGANISM
Phytolacca americana
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
1

REFERENCE
AUTHORS
Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE
Plant cell death system
JOURNAL
Patent: WO 0233107-A 7 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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Location/Qualifiers
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/organism="Phytolacca americana"
/db_xref="taxon:3527"
misc_feature
1..3
/note="Initiation codon added via PCR primer"
misc_feature
331..333
/note="Stop codon added via PCR primer"
BASE COUNT
106 a 63 c 76 g 88 t
ORIGIN

Query Match
Best Local Similarity 34.8%; Score 329; DB 6; Length 333;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 GGAGTTGATTCATCCCTGTAATAACTGAGGCTTTTCTACTGCTAGCCATCCAAATG 591
DB 4 GGAGTTGATTCATCCCTGTAATAACTGAGGCTTTTCTACTGCTAGCCATCCAAATG 53

QY 592 GTTTCAGAGGAGCGCGATTCAGTACATAGACCAAGTCAAGACTAATTTTAATAGA 551
DB 64 GTTTCAGAGGAGCGCGATTCAGTACATAGACCAAGTCAAGACTAATTTTAATAGA 123

QY 652 GCATTCTACCTGATCCCAAGTAAATTTGAGGAGAGAGTGGGGCAAAATCTCTGAG 711
DB 124 GCATTCTACCTGATCCCAAGTAAATTTGAGGAGAGAGTGGGGCAAAATCTCTGAG 183

QY 712 GCAATTCACAATGCCAAGTGGGCTTTTACCAAAACCACCTTGAGCTAGTGATGCCAAA 771
DB 184 GCAATTCACAATGCCAAGTGGGCTTTTACCAAAACCACCTTGAGCTAGTGATGCCAAA 243

QY 772 GGTACCAAGTGGATGTTCTTAGAGTGGATGAATCAATCTGATGGGCACTCCTTAAG 831
DB 244 GGTACCAAGTGGATGTTCTTAGAGTGGATGAATCAATCTGATGGGCACTCCTTAAG 303

QY 832 TACGTTAATGAACCTGTGCAGACACTTA 860
DB 304 TACGTTAATGAACCTGTGCAGACACTTA 332

RESULT 8
AX427716
LOCUS
AX427716
DEFINITION
Sequence 15 from Patent WO0233107.
ACCESSION
AX427716
VERSION
AX427716.1 GI:21537825
KEYWORDS
synthetic construct.
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE
Plant cell death system
JOURNAL
Patent: WO 0233107-A 15 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Location/Qualifiers
1..42
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/db_xref="taxon:32630"
/note="PSXDF primer"
15..20
variation
12 a 12 c 9 g 9 t
BASE COUNT
12 a 12 c 9 g 9 t

SOURCE
ORGANISM
Phytolacca americana
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
1

REFERENCE
AUTHORS
Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE
Plant cell death system
JOURNAL
Patent: WO 0233107-A 7 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Location/Qualifiers
1..333
/organism="Phytolacca americana"
/db_xref="taxon:3527"
misc_feature
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/note="Initiation codon added via PCR primer"
misc_feature
331..333
/note="Stop codon added via PCR primer"
BASE COUNT
106 a 63 c 76 g 88 t
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Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 64 GTTTCAGAGGAGCGCGATTCAGTACATAGACCAAGTCAAGACTAATTTTAATAGA 123

QY 652 GCATTCTACCTGATCCCAAGTAAATTTGAGGAGAGAGTGGGGCAAAATCTCTGAG 711
DB 124 GCATTCTACCTGATCCCAAGTAAATTTGAGGAGAGAGTGGGGCAAAATCTCTGAG 183

QY 712 GCAATTCACAATGCCAAGTGGGCTTTTACCAAAACCACCTTGAGCTAGTGATGCCAAA 771
DB 184 GCAATTCACAATGCCAAGTGGGCTTTTACCAAAACCACCTTGAGCTAGTGATGCCAAA 243

QY 772 GGTACCAAGTGGATGTTCTTAGAGTGGATGAATCAATCTGATGGGCACTCCTTAAG 831
DB 244 GGTACCAAGTGGATGTTCTTAGAGTGGATGAATCAATCTGATGGGCACTCCTTAAG 303

QY 832 TACGTTAATGAACCTGTGCAGACACTTA 860
DB 304 TACGTTAATGAACCTGTGCAGACACTTA 332

RESULT 8
AX427716
LOCUS
AX427716
DEFINITION
Sequence 15 from Patent WO0233107.
ACCESSION
AX427716
VERSION
AX427716.1 GI:21537825
KEYWORDS
synthetic construct.
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE
Plant cell death system
JOURNAL
Patent: WO 0233107-A 15 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Location/Qualifiers
1..42
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PSXDF primer"
15..20
variation
12 a 12 c 9 g 9 t
BASE COUNT
12 a 12 c 9 g 9 t

ORIGIN

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Best Local Similarity 4.4%; Score 42; DB 6; Length 42;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 CCTTTACCCAAACCACTTGAGCTAGCTAGTGCATGCCAAAGGTACC 777
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RESULT 9
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LOCUS
AX427717
DEFINITION
Sequence 16 from Patent WO0233107.
ACCESSION
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VERSION
AX427717.1 GI:21537826
KEYWORDS
synthetic construct.
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE
Plant cell death system
JOURNAL
Patent: WO 0233107-A 16 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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1..42
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/db_xref="taxon:32630"
/note="PSXDF primer"
22..27
variation
9 a 10 c 11 g 12 t
BASE COUNT
9 a 10 c 11 g 12 t
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QY 735 GGCTTTACCCAAACCACTTGAGCTAGCTAGTGCATGCCAAAGGTACC 776
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RESULT 10
AB071854
LOCUS
AB071854
DEFINITION
Phytolacca americana papsl gene for PAP-S1, partial cds.
ACCESSION
AB071854
VERSION
AB071854.1 GI:19570837
KEYWORDS
Phytolacca americana DNA.
SOURCE
Phytolacca americana
ORGANISM
Phytolacca americana
REFERENCE
1
AUTHORS
Honjo, E. and Watanabe, K.
TITLE
Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 783)
AUTHORS
Watanabe, K. and Honjo, E.
TITLE
Direct Submission
JOURNAL
Submitted (19-SEP-2001) Keio University, Saga University,
Department of Applied Biological Sciences; Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watake@acc.saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)
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DB 418 GGAATTCAACTCAGCAGTGCATTCGAAATCTCTCGA 459
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RESULT 11
LOCUS E05033 2472 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding antiviral protein.
ACCESSION E05033
VERSION E05033.1 GI:2173227
KEYWORDS JP 1993137580-A/1.
SOURCE Phytolacca americana.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 2472)
AUTHORS Kataoka,J., Habuka,N., Masuda,O., Miyano,M. and Koizumi,A.
TITLE NEW PROTEIN AND GENE CAPABLE OF CODING THE SAME
JOURNAL JAPAN TOBACCO INC
COMMENT OS Phytolacca americana
PN JP 1993137580-A/1
PD 01-JUN-1993
PF 20-NOV-1991 JP 1991329672
PI KATAOKA JIRO, HABUKA NORIYUKI, MASUDA OSAMU, MIYANO MASASHI,
PC KOIWAI AKIRA
PC C12N15/29,C12N15/73,C12P21/02//C12N1/21,(C12P21/02,C12R1/19),
PC (C12N1/21,
PC C12R1/19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Feature is identified by similarity;
FH Key Location/Qualifiers
FT CAAT_signal 549..552
FT CAAT_signal 627..630
FT TATA_signal 845..850
FT sig_peptide 1014..1085
FT mat_peptide 1086..1895
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BASE COUNT 272 a 159 c 153 g 199 t
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Query Match 4.4% Score 42; DB 8; Length 783;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 493 GGAATTCAACTCAGCAGTGCATTCGAAATCTCTCGA 534
|||||
DB 418 GGAATTCAACTCAGCAGTGCATTCGAAATCTCTCGA 459
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RESULT 11
LOCUS E05033 2472 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding antiviral protein.
ACCESSION E05033
VERSION E05033.1 GI:2173227
KEYWORDS JP 1993137580-A/1.
SOURCE Phytolacca americana.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 2472)
AUTHORS Kataoka,J., Habuka,N., Masuda,O., Miyano,M. and Koizumi,A.
TITLE NEW PROTEIN AND GENE CAPABLE OF CODING THE SAME
JOURNAL JAPAN TOBACCO INC
COMMENT OS Phytolacca americana
PN JP 1993137580-A/1
PD 01-JUN-1993
PF 20-NOV-1991 JP 1991329672
PI KATAOKA JIRO, HABUKA NORIYUKI, MASUDA OSAMU, MIYANO MASASHI,
PC KOIWAI AKIRA
PC C12N15/29,C12N15/73,C12P21/02//C12N1/21,(C12P21/02,C12R1/19),
PC (C12N1/21,
PC C12R1/19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Feature is identified by similarity;
FH Key Location/Qualifiers
FT CAAT_signal 549..552
FT CAAT_signal 627..630
FT TATA_signal 845..850
FT sig_peptide 1014..1085
FT mat_peptide 1086..1895
FT /product="antiviral protein"
FT CDS 1014..1898
FT polyA_site 2130..2135.
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1. 2472
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06/02/2003
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DB 1587 GTAGCCATCAATGCTTTTCAGAGGCGCGCG 1618
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RESULT 12
LOCUS PTCAPAP 2472 bp DNA linear PLN 01-FEB-2000
DEFINITION P. americana DNA for alpha-PAP(pokeweed antiviral protein).
complete cds.
ACCESSION D10600 D90537
VERSION D10600.1 GI:218010
KEYWORDS alpha-PAP; antiviral protein; pokeweed antiviral protein (PAP);
ribosome-inactivating protein.
SOURCE Phytolacca americana DNA.
ORGANISM Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 2472)
AUTHORS Kataoka,J., Habuka,N., Masuda,C., Miyano,M. and Koizumi,A.
TITLE Isolation and analysis of a genomic clone encoding a pokeweed
antiviral protein
JOURNAL Plant Mol. Biol. 20 (5), 879-886 (1992)
MEDLINE 93099240
REFERENCE 2 (bases 1 to 2472)
AUTHORS Kataoka,J.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1991) Jiro Kataoka, Japan Tobacco Inc., Life
Science Research Laboratory, 6-2 Umegakoka, Midori-ku, Yokohama,
Kanagawa 227, Japan (Tel:045-972-5901, Fax:045-972-6205)
COMMENT Submitted (23-Oct-1991) to DDBJ by:
Jiro Kataoka
Life Science Research Laboratory
Japan Tobacco Inc.
6-2 Umegakoka, Midori-ku
Yokohama 227
Japan
Phone: 045-972-5901
Fax: 045-972-6205.
FEATURES
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mat_peptide 1086..1895
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BASE COUNT 864 a 375 c 463 g 770 t
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Query Match 3.4% Score 32; DB 8; Length 2472;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 577 GTAGCCATCAATGCTTTTCAGAGGCGCGCG 608
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DB 1587 GTAGCCATCAATGCTTTTCAGAGGCGCGCG 1618
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 DEFINITION Sequence 13 from Patent WO0233107.
 ACCESSION AX427714
 VERSION AX427714.1 GI:21537823
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Neelam.A., Atkinson.H.J., Mcpherson.M.J. and Thomas.C.J.R.
 TITLE Plant cell death system
 JOURNAL Patent: WO 0233107-A 13 25-APR-2002;
 CAMBRIDGE ADVANCED TECH (GB)
 FEATURES
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 DB 23 GGAGTTGATTCATTCCTGTAATAACTGAG 52
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 LOCUS AY049785 1164 bp mRNA linear PLN 23-OCT-2001
 DEFINITION Phytolacca acinosa anti-viral protein PAP (PAP) mRNA, complete cds.
 ACCESSION AY049785
 VERSION AY049785.1 GI:16356654
 KEYWORDS Phytolacca acinosa.
 SOURCE Phytolacca acinosa.
 ORGANISM Phytolacca acinosa.
 REFERENCE 1
 AUTHORS Peng.X., Yuan.J. and Qiang.B.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUL-2001) Department of Biochemistry, Institute of Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, P.R. China
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 DB 23 GGAGTTGATTCATTCCTGTAATAACTGAG 52

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 DB 912 CTAATCTGGTGATCTATTTCAGGATTCCT 941
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 DEFINITION P.americana PAP gene for anti-viral protein.
 ACCESSION X55383
 VERSION X55383.1 GI:20421
 KEYWORDS antiviral protein; cell wall protein; PAP gene; ribosome;
 inactivating protein.
 SOURCE Phytolacca americana.
 ORGANISM Phytolacca americana.
 REFERENCE 1
 AUTHORS Antoniw,J.F.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops Research, Dept. of Plant Pathology, Rothamsted Experimental Station, Harpenden, Hert, AL5 2JQ, UK
 2 (bases 1 to 1164)
 REFERENCE 2
 AUTHORS Lin.Q., Chen.Z.C., Antoniw,J.F. and White,R.F.
 TITLE Isolation and characterization of a cDNA clone encoding the anti-viral protein from Phytolacca americana
 JOURNAL Plant Mol. Biol. 17 (4), 609-614 (1991)
 MEDLINE 92003676
 PUBMED 1912488
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 DB 913 TAATCTGGTGATCTATTTCAGGATTCCT 941

Mon Jun 2 10:54:54 2003

Search completed: June 2, 2003, 04:16:54
Job time : 2637 secs

09978274

SRNT

Printed: 11/17/2004

us-09-978-274a-1.oli.rge

Page 9

06/02/2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 03:17:33 ; Search time 1674 Seconds

(without alignments)
9142.613 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: em_estpl:*

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8: em_hic:*

9: gb_estl:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	23	2.4	621	17	AZ551992 RPCI-23-2
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C 4	20	2.1	333	9	A1426126 mj15g05.x
C 5	20	2.1	356	10	BE626842 ut85b04.x
C 6	20	2.1	359	17	U68743 U68743 Rft

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C 8	20	2.1	404	13	BM124309
C 9	20	2.1	406	9	AT846009
C 10	20	2.1	410	14	HQ299989
C 11	20	2.1	428	17	AZ066860
C 12	20	2.1	474	10	BE533559
C 13	20	2.1	486	13	BM124329
C 14	20	2.1	489	5	AA058263
C 15	20	2.1	498	17	AZ512811
C 16	20	2.1	510	17	AZ931405
C 17	20	2.1	522	12	HQ074442
C 18	20	2.1	529	9	AI509974
C 19	20	2.1	618	10	AW553340
C 20	20	2.1	757	17	AZ791282
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C 22	20	2.1	833	13	BM041411
C 23	20	2.1	840	17	BH592738
C 24	20	2.1	969	12	BG331808
C 25	20	2.1	1808	11	AK017874
C 26	19	2.0	102	12	BF802805
C 27	19	2.0	348	9	AI702931
C 28	19	2.0	394	7	AZ739560
C 29	19	2.0	433	17	AQ041218
C 30	19	2.0	434	10	BE210307
C 31	19	2.0	437	10	BE555213
C 32	19	2.0	450	17	AQ498030
C 33	19	2.0	456	12	RG348196
C 34	19	2.0	466	9	AA188413
C 35	19	2.0	495	10	BE331524
C 36	19	2.0	521	12	RG307366
C 37	19	2.0	569	17	BH773398
C 38	19	2.0	576	14	BM732577
C 39	19	2.0	581	17	AZ863325
C 40	19	2.0	599	17	BH774064
C 41	19	2.0	603	17	BH711448
C 42	19	2.0	651	17	AZ507759
C 43	19	2.0	697	10	BE403742
C 44	19	2.0	708	10	BE646599
C 45	19	2.0	791	17	BH024114

ALIGNMENTS

RESULT 1
A0706592/c
LOCUS
DEFINITION
HS_5533_B2_C03_SP6E RPCI-JJ Human Male BAC Library Homo sapiens
VERSION
A0706592
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 360)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.U. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-JJ. For BAC
library availability, please contact Pieter de Jong

360 bp DNA linear GSS 07-JUL-1999

Genomic clone Plate-1109 Col-6 Row-F, DNA sequence.

GI:5416018

(pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 1109 row: F column: 6
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 360.

FEATURES

Location/Qualifiers
 1..360
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=1109 Col=6 Row=F"
 /clone_lib="RPC1-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
 BASE COUNT 100 a 58 c 54 g 148 t
 ORIGIN

Query Match 2.4% Score 23; DB 17; Length 360;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 CAACCTAAACATTACACTA 264
 ||||||||||||||||||
 DB 50 CAACCTAAACATTACACTA 28

RESULT 2

AZ551992 621 bp DNA linear CSS 20-NOV-2000
 LOCUS RPC1-23-210L20.TJ RPC1-23 Mus musculus genomic clone RPC1-23-210L20
 DEFINITION DNA sequence.
 ACCESSION AZ551992
 VERSION AZ551992.1 GI:11231492
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 621)
 REFERENCE Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPC1-23
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPC1-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 210 row: L column: 20
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..621
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPC1-23-210L20"

/clone_lib="RPC1-23"
 /sex="Female"
 /lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 209 a 88 c 102 g 222 t
 ORIGIN

Query Match 2.4% Score 23; DB 17; Length 621;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 884 TTATAATTCTACTTATTATAAT 906
 ||||||||||||||||||
 DB 247 TTATAATTCTACTTATTATAAT 269

RESULT 3

AZ243043 171 bp DNA linear CSS 15-JUN-2000
 LOCUS RPC1-23-36G6.TJB RPC1-23 Mus musculus genomic clone RPC1-23-36G6,
 DEFINITION DNA sequence.
 ACCESSION AZ243043
 VERSION AZ243043.1 GI:8556234
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 171)
 REFERENCE Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPC1-23
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPC1-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 36 row: G column: 6
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..171
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPC1-23-36G6"
 /clone_lib="RPC1-23"
 /sex="Female"
 /lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 35 a 67 c 23 g 46 t

Query Match 2.1% Score 20: DB 17: Length 171:

Best Local Similarity 100.0%: Pred. No. 20: Mismatches 0: Indels 0: Gaps 0:

Matches 20: Conservative 0:

Oy 684 GGAGGAGAGTGGGGCAAA 703

Db 153 GCAGGAGAGTGGGGCAAA 134

RESULT 4

BE626842/c

LOCUS

DEFINITION

clone IMAGE:476216 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

1 (bases 1 to 333)

Underwood, K., Steptoe, M., Theising, B., Allen, M., Powers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

Waterston, R., and Wilson, R.

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL: contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

High quality sequence stop: 286.

Location/Qualifiers

1..333

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:476216"

/sex="unknown"

/tissue_type="embryo"

/dev_stage="13.5-14.5dpc total fetus"

/lab_host="DH10B"

/note="vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5,

TGTTACCAATCTGAAGTCGAGCCGCCGCGAAATTTTTTTTTTTTTTTTTTT

T 3'], on equal amounts of mRNA from 2 13.5dpc and 2

14.5dpc embryos [total RNA provided by Minoru Ko, Wayne

State Univ., from 2]; double-stranded cDNA was ligated to

Eco RI adaptors (Pharmacia). digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pT7T3 vector. Library went through one round of

normalization, and was constructed by Bento Soares and

M.Fatima Bonaldo."

114 a 58 c 62 g 99 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%: Pred. No. 21:

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 120 TGCACCTTTATGGAATCTC 139

Db 320 TGCACCTTTATGGAATCTC 301

RESULT 5

BE626842/c

LOCUS

DEFINITION

ut85b04.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone

IMAGE:3369199 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 356)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other ESUs: ut85b04.y1

Contact: Robert Stransberg, Ph.D.

Email: cchapos-r@mail.nih.gov

This clone is available royalty-free through LNL: contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

High quality sequence stop: 346.

Location/Qualifiers

1..356

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:3369199"

/clone_lib="Soares_mammary_gland_NMLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker. 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT7T3 vector. Library is normalized. Library

was constructed by Bento Soares and M. Fatima Bonaldo."

117 a 61 c 66 g 112 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%: Pred. No. 21:

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 120 TGCACCTTTATGGAATCTC 139

Db 336 TGCACCTTTATGGAATCTC 317

RESULT 6

U68743/c

LOCUS

DEFINITION

U68743 Rittia pachyptila anonymous nuclear DNA Rittia pachyptila

genomic clone pUKP113.1F, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 359)

Karl, S.A. and Wawrik, B.

Identification of potentially functional regions in anonymous

BF626842

ut85b04.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone

IMAGE:3369199 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 356)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other ESUs: ut85b04.y1

Contact: Robert Stransberg, Ph.D.

Email: cchapos-r@mail.nih.gov

This clone is available royalty-free through LNL: contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

High quality sequence stop: 346.

Location/Qualifiers

1..356

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:3369199"

/clone_lib="Soares_mammary_gland_NMLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker. 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT7T3 vector. Library is normalized. Library

was constructed by Bento Soares and M. Fatima Bonaldo."

117 a 61 c 66 g 112 t

BASE COUNT

ORIGIN

Query Match 2.1% Score 20: DB 10: Length 356;

Best Local Similarity 100.0%: Pred. No. 21:

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 120 TGCACCTTTATGGAATCTC 139

Db 336 TGCACCTTTATGGAATCTC 317

RESULT 6

U68743/c

LOCUS

DEFINITION

U68743 Rittia pachyptila anonymous nuclear DNA Rittia pachyptila

genomic clone pUKP113.1F, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 359)

Karl, S.A. and Wawrik, B.

Identification of potentially functional regions in anonymous

BF626842

ut85b04.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone

IMAGE:3369199 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 356)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other ESUs: ut85b04.y1

Contact: Robert Stransberg, Ph.D.

Email: cchapos-r@mail.nih.gov

This clone is available royalty-free through LNL: contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

High quality sequence stop: 346.

Location/Qualifiers

1..356

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:3369199"

/clone_lib="Soares_mammary_gland_NMLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker. 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pT7T3 vector. Library is normalized. Library

was constructed by Bento Soares and M. Fatima Bonaldo."

117 a 61 c 66 g 112 t

BASE COUNT

ORIGIN

Query Match 2.1% Score 20: DB 10: Length 356;

Best Local Similarity 100.0%: Pred. No. 21:

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 120 TGCACCTTTATGGAATCTC 139

Db 336 TGCACCTTTATGGAATCTC 317

RESULT 6

U68743/c

LOCUS

DEFINITION

U68743 Rittia pachyptila anonymous nuclear DNA Rittia pachyptila

genomic clone pUKP113.1F, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 359)

nuclear DNA sequences from a variety of metazoans
 Unpublished (1996)
 Contact: Karl SA
 Biology
 University of South Florida
 4202 East Fowler Ave., LIF 136, Tampa, FL 33620, USA
 Email: karl@chuma.ces.usf.edu
 Class: unknown

FEATURES

Source
 1. 359

/organism="Riftia pachyptila"

/db_xref="taxon:6426"

/clone="pdrptl13.1f"

/clone_lib="Riftia pachyptila anonymous nuclear DNA"

119 a 65 c 49 g 119 t 7 others

BASE COUNT

ORIGIN

Query Match 2.1% Score 20; DB 17; Length 359;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE847234

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE847234

LOCUS

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VERSION

KEYWORDS

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REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE847234

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

RESULT 10
BQ299989
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

MR1-KT0058-191200-007-c10 KT0058 Homo sapiens cDNA, mRNA sequence.
BQ299989 410 bp mRNA linear EST 16-MAY-2002
BQ299989 1 GI:20815511
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

1 (bases 1 to 410)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, M.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MK12-MR1-KT0058-
191200-007-c10&t3=2000-12-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 41.
Location/Qualifiers
1..410
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KT0058"
/dev_stage="Adult"
/note="Organ: bladder_tumor; Vector: puc18; Site: 1; SmaI:
Site_2: SmaI: A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 100 a 111 c 101 g 98 t
ORIGIN

Query Match 2.1% Score 20; DB 14; Length 410;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GATCACCCTTTGATGCTGGAA 100
|||||
Db 297 GATCACCCTTTGATGCTGGAA 316

RESULT 11
A2066860/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

A2066860 428 bp DNA linear GSS 30-MAR-2000
RPECJ-23-434M3.TJ RPECJ-23 Mus musculus genomic clone RPECJ-23-434M3,
DNA sequence.
A2066860
A2066860.1 GI:7358112
GSS.
house mouse.
Mus musculus

DB 325 TCCACCTTTTGGATCTC 306
|||||
A1846009 406 bp mRNA linear EST 15-JUL-1999
UI-M-API-agl-e-12-0-UI-3' NIH_BMAP_MST_N Mus musculus cDNA clone
UI-M-API-agl-e-12-0-UI 3', mRNA sequence.
A1846009 1 GI:5489915
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
Bonald, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@nhi.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized corpus striatum library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..406
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UI-M-API-agl-e-12-0-UI"
/clone_lib="NIH_BMAP_MST_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_MST_N library is a normalized library constructed
from mouse striatum. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonald,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Ms. Annie Novakovich, Zivic-Miller
Laboratories.
TAG_LIB=NIH_BMAP_MST_N
TAG_TISSUE=corpus-striatum
TAG_SEQ=ACGGC"
BASE COUNT 138 a 75 c 84 g 109 t
ORIGIN

Query Match 2.1% Score 20; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 TCCACCTTTTGGATCTC 139
|||||
Db 313 TCCACCTTTTGGATCTC 294

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 428)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Kroll, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-433M3.TV
Contact: Shaving Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaod@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
or from Resea ch Genetics (inforesgen.com). BAC end page:
http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
plate: 433 row: M column: 3
Seq primer: SP6
Class: BAC ends.

TITLE
JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1..428
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-433M3"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 82 a 141 c 76 g 129 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 GGAGGAGAGTGGGGCAAAA 703
Db 172 GGAGGAGAGTGGGGCAAAA 153

RESULT 12
BE553559
LOCUS
DEFINITION
UI-M-Ap1-agi-e-12-0-UI.r1 NIH_BMAP_MST_N Mus musculus cDNA clone
UI-M-Ap1-agi-e-12-0-UI 5', mRNA sequence.
ACCESSION
BE553559.1 GI:9979466
VERSION
BE553559.1
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 474)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
COMMENT
Contact: Chin, H
National Institute of Mental Health

Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 GGAGGAGAGTGGGGCAAAA 703
Db 172 GGAGGAGAGTGGGGCAAAA 153

RESULT 12
BE553559
LOCUS
DEFINITION
UI-M-Ap1-agi-e-12-0-UI.r1 NIH_BMAP_MST_N Mus musculus cDNA clone
UI-M-Ap1-agi-e-12-0-UI 5', mRNA sequence.
ACCESSION
BE553559.1 GI:9979466
VERSION
BE553559.1
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 474)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
COMMENT
Contact: Chin, H
National Institute of Mental Health

Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 684 GGAGGAGAGTGGGGCAAAA 703
Db 172 GGAGGAGAGTGGGGCAAAA 153

RESULT 12
BE553559
LOCUS
DEFINITION
UI-M-Ap1-agi-e-12-0-UI.r1 NIH_BMAP_MST_N Mus musculus cDNA clone
UI-M-Ap1-agi-e-12-0-UI 5', mRNA sequence.
ACCESSION
BE553559.1 GI:9979466
VERSION
BE553559.1
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 474)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
COMMENT
Contact: Chin, H
National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mst@mail.nih.gov

CDNA Library Preparation: M.B. Soares Lab Clone Distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS, it
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
Location/Qualifiers
1..474
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-Ap1-agi-e-12-0-UI"
/clone_lib="NIH_BMAP_MST_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_MST_N library is a normalized library constructed
from mouse striatum. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Ms. Annie Novakovich, Zivir-Miller
Laboratories."

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source

Location/Qualifiers
1..474
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-Ap1-agi-e-12-0-UI"
/clone_lib="NIH_BMAP_MST_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pMT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_MST_N library is a normalized library constructed
from mouse striatum. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dT track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Ms. Annie Novakovich, Zivir-Miller
Laboratories."

BASE COUNT 104 a 160 c 95 g 115 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 TGCACCTTTATGGAATCTC 139
Db 380 TGCACCTTTATGGAATCTC 399

RESULT 13
BM124329/c

LOCUS
DEFINITION
L0538E12-3 NIA Mouse Newborn Heart cDNA Library Mus musculus cDNA
clone L0538E12 3', mRNA sequence.
ACCESSION
BM124329.1 GI:17108097
VERSION
BM124329.1
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 486)
Piao, Y., Kargul, G.J., Dudekula, D.B., Olan, Y., Pantano, S., Lim, M.K.
and Ko, M.S.H.
Systematic Analyses of NIA Mouse Newborn Heart cDNA Library
Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lysun-grc.nia.nih.gov
Plate: L0538 row: E column: 12
Seq primer: -21M13 Forward
High quality sequence stop: 486
polyA-Yes.

FEATURES
source

Location/Qualifiers
1..486
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:L0538E12-3"

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

Location/Qualifiers
1..486
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:L0538E12-3"

FEATURES
source

Location/Qualifiers
1..486
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:L0538E12-3"

```

/db_xref="taxon:10090"
/clone_lib="NIA Mouse Newborn Heart cDNA Library"
/tissue_type="Newborn Heart"
/dev_stage="Newborn"
/lab_host="DH10B"
/notes="Organ: heart; vector: pSPORT1 (Invitrogen); Site_1:
SalI; Site_2: NotI; Mouse cDNA project by the Laboratory
of Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen, 5'-
GACTAGTCTAGATCGGAGCGCGCCCTTTT-3') from
24.9 microgram of total RNA, treated with RNase
polymerase, and purified by ethanol-precipitation. The
cDNAs were ligated to Loe-linker LL-Sal3 (Ref.
Development 127:1737-1749 (2000) PMID: 107252491),
purified by phenol/chloroform, and separated from free
linkers by Centricon 100. Then, the cDNAs were digested
with SalI and NotI enzymes, and cloned into SalI and NotI
site of pSPORT1 plasmid vector. The DH10B E. coli host was
transformed with ligation mixture by the chemical method.
The average insert size is about 1.8 kb. The library was
constructed by Yulan Piao (NIA)."
BASE COUNT      153 a   97 c   114 g   122 t
ORIGIN
Query Match      2.1%; Score 20; DB 13; Length 486;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 120 TGCACCTTTATGGAATCTC 139
      |||||||
Db 325 TGCACCTTTATGGAATCTC 306

RESULT 14
AA058263
LOCUS      489 bp      mRNA      linear      EST 19-SEP-1996
DEFINITION clone IMAGE:480339 5', mRNA sequence.
VERSION     AA058263.1 GI:1551098
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 489)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:291083
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 464.
Location/Qualifiers
1..489
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

```

```

/clone="IMAGE:480339"
/clone_lib="Soares mouse embryo NBMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="vector: pTT30-pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; 3st strand cDNA
was primed with a NotI - oligo(dT) primer 15'-
TGTTCATCTCAACTGCGAGCGCGCGGAAATTTT-3'.
T 3', on equal amounts of mRNA from 2 14.5dpc and 2
14.5dpc embryos [total RNA provided by Minou K. Wayne
State Univ., from 2 1; double-stranded cDNA was ligated to
EcoRI adaptors (Pharmacia), digested with NotI and
cloned into the NotI and EcoRI sites of the modified
pTT30 vector. Library went through one round of
normalization, and was constructed by Renato Soares and
M. Fatima Bonaldo."
BASE COUNT      92 a   176 c   102 g   119 t
ORIGIN
Query Match      2.1%; Score 20; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 120 TGCACCTTTATGGAATCTC 139
      |||||||
Db 466 TGCACCTTTATGGAATCTC 485

RESULT 15
AA0512831
LOCUS      498 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION clone UUCIM0358K09 R, DNA sequence.
VERSION     AA051283.1 GI:10694147
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 498)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Humil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Kelly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhansern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 Std error: 0.00
Plate: 0358 row: K column: 09
Seq primer: CACACAGGAACACGATGACG
Class: plasmid ends
High quality sequence stop: 498.
Location/Qualifiers
1..498
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUCIM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/notes="vector: PWD42nv; Purified genomic DNA from M.

```


musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 150 a 96 c 91 g 161 t

ORIGIN

Query Match 2.11; Score 20; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 249 AAAAACCATTACACTATGTC 268
Db 397 AAAAACCATTACACTATGTC 416

Search completed: June 2, 2003, 04:50:14
Job time : 1679 secs


```

BASE COUNT      147 a      99 c      86 g      229 t
ORIGIN

Query Match      4.5% Score 42.4; DB 17; Length 561;
Best Local Similarity 51.0%; Pred. No. 2.6;
Matches 100; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 145 AATCAAGCGAAGACATCAAAATGCTATGGCATACCAATGGTACCTGATACAT 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 AATTATAAAATTTATCAAAAATATCAACAATGAATTAATAAATTTATACAT 333

QY 205 TCGACCCCTTAAGTCTATTTGGTTAAGCTCCAGGTGCAACCTAAACCATTA 264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 TCCAAACCAACCAATTTACTCAACCAAAACAATGGTAACTTACCTATCAAC 273

QY 265 ATCTGAGACGAATACCTTATACGTGATGGTATTTCTGATCCCTCAATG 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 ATCCGCAATATACATCATTTCTTTTTCCTCAAACTCTCTCTTTTTC 213

QY 325 TGTGTTTACCATATAT 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 TTGCTTTTCTTAAT 197

RESULT 13
CNS0039G/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL063921
VERSION
AL063921.1 GI:4941778
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster.
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
COMMENT
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Osoegawa and
Aaron Mammosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone.lib="RPCI-98"
/note="end : TET3"
BASE COUNT      201 a      64 c      131 g      202 t      503 others
ORIGIN

Query Match      4.5% Score 42.4; DB 17; Length 1101;
Best Local Similarity 19.6%; Pred. No. 3.1;
Matches 136; Conservative 262; Mismatches 285; Indels 11; Gaps 3;

QY 241 GCAACCTAAACACCATTTACACTAATGCTGAGACAAATAACTTATACGTGATGCTAT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1101 GAARRGGDDTDWDRDTHKKDDWMTKMTWKDRADRRWAGDADRWAMODUGCATTTAT 1042

QY 301 TCTGATCCCTTCAATGCGCAATAGTCTGCTTACCATTATTTTAATGATATTACACAC 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1041 WWWWMMATVDTWMDKWWMTAAKTDTAWTWRTAWRADWDRGAGKRDKDAATDA 984

QY 361 GAAGCGACTGATCTGAGAAATCTCTTTGCTCAAGTTCTAGTCTCTGCTGTTGCAAT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 983 -DAGRRDUGRRKDKDKDKDDDDKGGKKKKAACAATKWWDDWDDKDKKWDGAK 925

QY 421 ATTAACCTAATAGCTTATATCCGATCATGGAAGAAAGACAGATAACATCAAGAAAT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 924 DRKAFDDGAGKDDGKGGKDDDDTDTGTDKDDDDKDDWDDKAKGTGSDATWAAAT 805

QY 481 CAAGTCCAATTTGGGAATTCAAATACATCAGCAGTGACATTTGGAAAATCTCTGAG 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 864 WWSGADADWMTWDAADDDWADDDWADWADWADWADWADWADWADWADWADWAD 805

QY 541 TCAATCCCTGTAAACACTGAGGCTTTTCTTACTGCTAGCCATCCCAATGCTTACAG 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 804 KRDRKRADDKRDADDDDDATWTTTTRDODWKKWTWTWKAAADKTDWDDDD 745

QY 601 GCACGG-CAATCAAGTACATAGACACCAAGTCAAGACATAATTTAATAGACATCT 659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 744 DRDRAGTAGKKWRTWKRRKRRDTHWDDADDDTDRDRRRRGGDDCAACGCKTK 685

QY 660 CCCGATCCCAAGTAAATTAATTTGGAGGAGAGTGGGGCAAAATCTCTGAGCAAT 719
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 684 RRDRATWDRDADWADAAWMTTDTDDWDRRRRRKRRRRRTTAAGWAWW 625

QY 720 CAATGCCAAGATCGGGCTTTTACCACCAACCTAGCTAGTGCATGCCAAGATCT 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 624 WDNKWKWTKTRADWDR-----WAADTWTDARKADRWAKAKAKAKAKAKAD 572

QY 780 GTGATAGTTCTTAGAGTGTGATCAATCAATCAATGCTGAGTGGCACTCTTAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 571 RWTGKGTATTTATTTTAAAWAAWAAWATTTATTTTTTTTTTTTTTTTTT 512

QY 840 TGAACCTGTGACACAACTTACCAAAATGCCATGCTCTCCAAATTTCTACT 859
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 511 WWAHAWTATWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 452

QY 900 TTATAATTTATATGCTTAATCTCTGCTGATCTATT 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 451 TTTTAAWAAWTTTWTWTWTTTAAWAAWAAWAAWAAWAAWAAWAAWAAW 418

RESULT 14
CNS007BE
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR15H24 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL066953
VERSION
AL066953.1 GI:4945517
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster.
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1001)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
COMMENT
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Osoegawa and
Aaron Mammosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone.lib="RPCI-98"
/note="end : TET3"
BASE COUNT      201 a      64 c      131 g      202 t      503 others
ORIGIN

```


FORWARD: T7

BACKWARD: T3
Plate: L48-5 row: G column: 12
Seq primer: T3

High quality sequence stop: 350
POLYA=No.

FEATURES

source

Location/Qualifiers

1..489
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone="L48-484"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library", 48 hours NaCl treatment"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
EcoRI: 160 a 98 c 106 g 125 t

BASE COUNT

ORIGIN

Query Match 4.9% Score 46.6; DB 10; Length 489;

Best Local Similarity 54.7%; Pred. No. 0.2;
Matches 122; Conservative 0; Mismatches 89; Indels 12; Gaps 1;

QY

113 ACAATATGCCACCTTTATGGAACTCTTCGTAATCAAGCGAAGATCCAAACTAAAT 172

Db

196 ATACATACCATCATCTCCCTGGAATCTACGCAATCAACTGAAGGATCCCAATGACAAC 255

QY

173 GCTATGGCATACCAATGCTACCTGATCTACTAATTCGACCCC-----TAAGTACT 220

Db

256 CCATAGTATATACGATGCGCAAAACCTACGACTTCCAGATGGACAACGATACATATC 315

QY

221 TATTGGTTAAGTCCCAAGTGCAAACTAAAAACCATTAACATAATGCTGAGACGAATA 280

Db

316 TGTACTAGAGCTGCAGGCGAGCACCCAAAGGCCATCATATATCTCTAGACAGAACA 375

QY

281 ACTTATACGTGATGGCTATCTTCGATCCCTTCAATGGCAATA 323

Db

376 ATTATATTTCATGGCTACAGTGACATGGTATTGAAATAA 418

RESULT 9

AA856221

LOCUS

DEFINITION

AA856221 267 bp mRNA linear EST 20-FEB-2001
L30-242T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-242 5' similar to Ribosome inactivating protein precursor (antiviral protein), mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AA856221.1 GI:2944523
Common Iceplant.
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 267)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers

FORWARD: T7

BACKWARD: T3

Plate: L30-3 row: D column: 10
Seq primer: T3

FEATURES

source

High quality sequence stop: 230.

Location/Qualifiers

1..267
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone="L30-242"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library", 30 hours NaCl treatment"
/tissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
EcoRI: 85 a 48 c 69 g 65 t

BASE COUNT

ORIGIN

Query Match 4.8% Score 45.4; DB 9; Length 267;

Best Local Similarity 53.0%; Pred. No. 0.35;
Matches 97; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY

453 AAAGAAGCAGAGTAAGTAAACTCAAGAAATCAAGTCCCAATGGGAATTCAAATACACAGAG 512

Db

25 ACAGATCTCTGCAACCAACGACGACAGCCATAGAGTTAGGGTGGATAAATACAGATT 84

QY

513 TGACATTTGGAATATCTCTGGAGTTGATTCATTCCTGTAATAACTGAGGCTTTTCT 572

Db

85 TCGCATCGAGCTCGGTTTATGGTAAGACATCGACAGCAATGAGGCTAAATTCCT 144

QY

573 ACTGTTAGCATCCCAATGTTTTCAGACGCGCGGATTCAGTACATAGACAAATCACT 632

Db

145 GCTGATGTCATACAGATGTTTCTGAGCAGCAGGTTTCAAGTATATTGACAGTAAGCT 204

QY

633 CAA 635

Db

205 GAA 207

RESULT 10

BE036639

LOCUS

DEFINITION

BE036639 1021 bp mRNA linear EST 07-JUN-2000
MP03H03 MP Mesembryanthemum crystallinum cDNA 5' similar to ribosome-inactivating protein gelonin, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BE036639.1 GI:8331648
Common Iceplant.
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 1021)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers
1..1021
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_lib="Mp"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/note="3 d 500mM NaCl"

BASE COUNT

ORIGIN

302 a 242 c 235 g 241 t 1 Others

Db 313 GCTGATTCCTATACACATGCTTCTGAGCAGCAGCGTTTAAAGTATATTCAAAGTAAGGT 372
 QY 633 ---CAAGACTAATTTAATAGACATCTACCCCTGATCCCAAGTAAATTTTGGAGGA 689
 Db 373 GACCAAAAGTGGTTACATGCTGCTATACCCGACCGAAGAGTGTCACTTTTGGAGAA 432
 QY 690 GAAGTGGGGCAAAATCTCTGAGGCAATTCACA 721
 Db 433 CAATTGGGGGAAGATTTCGCAAGAGATTCATA 464

RESULT 4
 BE033546
 LOCUS
 DEFINITION MF03A09 MF Mesembryanthemum crystallinum cDNA 5' similar to
 ribosome-inactivating protein, mRNA sequence.
 ACCESSION BE033546
 VERSION BE033546.1 GI:8328555
 KEYWORDS EST.
 SOURCE common iceplant.
 ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Caryophyllales; Alzaceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 1038)
 AUTHORS Bohnert, H.J., Borchert, C., Brazill, S., Brooks, J., Eaton, M., Ferrer,
 H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,
 Seara, G., Wheeler, M. and Zepeda, C.R.
 TITLE Functional Genomics of Plant Stress Tolerance
 JOURNAL Unpublished (2000)
 COMMENT Contact: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu
 An open reading frame exists.
 FEATURES
 source
 1. 1038
 Location/Qualifiers
 /organism="Mesembryanthemum crystallinum"
 /db_xref="taxon:3544"
 /clone_lib="MF"
 /tissue_type="Root"
 /dev_stage="5-6 weeks old"
 /note="vector: Bluescript SK+; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 232 a 259 c 183 g 363 t 1 others
 Query Match 5.9%; Score 55.4; DB 10; Length 1038;
 Best Local Similarity 52.7%; Pred. No. 0.0013;
 Matches 144; Conservative 0; Mismatches 126; Indels 3; Gaps 1;
 QY 453 AAGAAAGCAGCAAGTAACCAAGCAAGTCAATTCGAATTCGAATTCGAATTCAGGAG 512
 Db 286 AGAAGAGCGTGCAGCAAGCAAGCGCAATTCGAATTCGAATTCGAATTCAGGAGT 345
 QY 513 TGCAATTCGAAATATCTCTGGAGTTGATTCATTCCTCTTAAATCTGAGGCGTTTCT 572
 Db 346 CGCATCGAGTCGGTTTTGGTAGACCCCAATTAATGGCGAGTGGAGGCCAATTCCT 405
 QY 573 ACTGGTAGCCATCAATGGTTTCAGAGCGAGCGGATTCGAATTCGAATTCGAATTCAGG 632
 Db 406 GCTATTGCTATACAGATGGTTCTGAGCAGCAGCGTTTAAAGTTTATTGAAAGTAAAGT 465
 QY 633 CA---AGACTAATTTAATAGACATCTCTACCCCTGATCCCAAGTAAATTTTGGAGCA 689
 Db 466 GACCAAAAGTGGTGTACATGCTGTTTCAAAACCCGACCGAAGAGTGTGAGTTCGGTGA 525
 QY 690 GAAGTGGGGCAAAATCTCTGAGGCAATTCACA 722
 Db 526 CAATTGGGTGAACATTTTCCATGAGACTCATAA 558

RESULT 5

LOCUS T24255
 DEFINITION crs1345 lambdaZAPST Ricinus communis cDNA clone pcrs1345, mRNA
 sequence.
 ACCESSION T24255
 VERSION T24255.1 GI:689074
 KEYWORDS EST.
 SOURCE castor bean.
 ORGANISM Ricinus communis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids 1; Malpighiales; Euphorbiaceae; Ricinus.
 REFERENCE 1 (bases 1 to 405)
 AUTHORS VandeOo, F.J., Turner, S. and Somerville, C.
 TITLE Expressed sequence tags from developing castor seeds
 JOURNAL Plant Physiology, 108, 1141-1150 (1995)
 COMMENT Contact: Somerville CR
 Carnegie Institution
 Carnegie Institution, 290 Panama St, Stanford, CA 94305
 Tel: 415/2531521
 Email: crs@andrew.stanford.edu
 Seq primer: T3.

FEATURES

source
 1. 405
 Location/Qualifiers
 /organism="Ricinus communis"
 /strain="Baker 296"
 /db_xref="taxon:3988"
 /clone_lib="pcrs1345"
 /note="vector: lambdaZAPST"
 /note="vector: lambdaZAPST; Site_1: EcoRI; Site_2: XhoI;
 Poly(A)+ RNA was purified from developing stage 111 to
 stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
 1982) endosperm plus embryo of immature castor fruits.
 cDNA was synthesized and cloned into lambdaZAPST according
 to the instructions of the manufacturer (Stratagene).
 synthesis was primed from the poly(A) tail, and cloned
 directionally into XhoI (3') and EcoRI (5') sites. In few
 cases, sequence data indicated that this directionality
 was reversed. Partial cDNA clones predomininate."
 BASE COUNT 118 a 84 c 86 g 110 t 7 others

Query Match 5.5%; Score 52.4; DB 14; Length 405;
 Best Local Similarity 59.2%; Pred. No. 0.006;
 Matches 125; Conservative 0; Mismatches 79; Indels 7; Gaps 2;

QY 555 AACTGAGGCTTTTCTTCTAGTGGTATGAGCATCAAAATGTTTCAGAGGAGCGGATTCAA 614
 Db 82 AACTCTGCGTCTGCTCTTATGTTTCATCCAAATGATTTCAAGCAGCAGCAATTCGA 141
 QY 615 CTACATGAGACACCAAGCTCAAGACTAATTTT-----AATAGACCATTCAGCTGATCC 668
 Db 142 GTACATTTCAGGAGAAATATGCGCAGAGATAGGTACACCCGAGATCTCCATCCATCC 201
 QY 669 CAAAGTAAATTAATTCGAGGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACA-ATGCA 727
 Db 202 TAGCGTAATTAACACTTNGAATAGTTGGGAGAGACTTCCACTGCAATTCAGAGCTA 261
 QY 728 AGAATGAGCTTTTACCCCAAACTTCAAGCT 758
 Db 262 ACCAAGGAGCTTTGCTAGTCCANTTCAACT 292

RESULT 6

LOCUS BE037217
 DEFINITION MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to
 ribosome-inactivating protein/antiviral protein, mRNA sequence.
 ACCESSION BE037217
 VERSION BE037217.1 GI:813233

```

/db_xref="taxon:3544"
/clone_lib="MM"
/cell_type="epidermal bladder cells"
/dev_stage="12 weeks old"
/notes="vector: Bluescript SK+; Site_1: EcoRI; Site_2: XhoI
; Plants stressed 6 weeks in 500mM NaCl"
BASE COUNT      283 a  220 c  203 g  287 t
ORIGIN

Query Match      9.2%  Score 87;  DB 10;  Length 993;
Best Local Similarity 60.1%  Pred. No. 7.8e-12;
Matches 163;  Conservative 0;  Mismatches 105;  Indels 3;  Gaps 1;

Oy  455 AGAAGCAGAGTAAACTCAAGAAATCAAGTCCCAATTCGAATTCGAATTCGAAGTGC 514
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  680 AGAAGCTGCGGTCAAGCAGAAACAGATATTGACGTTGGGGCTTCTTAATATACATTTG 621
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  515 ACATTGCAAAATCTCTGGAGTTCATTCATTCCTCTGAAACAGTGGGCTTTTTCCTAC 574
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  620 CCATCGAGTCAATTTATGTTAAACAAACAGATCGATGGAAACATCGAGGCCAAATTCCTAC 561
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  575 TGTAGTCCATCTCAAGTTCAGAGCAGCGGATTCAGTCAAGTACATACAGAACAAATTC 632
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  560 TGATGTCATCCAGATCGTTTCAGAGCAGCAGGTTCCATATATCGACACTAAGTGC 501
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  633 -CAAGACTAATTTTAATAGAGCATTCTACCTGATCCCAAGTAATTAATTTTACAGAGA 691
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  500 CGAAGTGGTCAATCGTTCTCAACCCGATCGAAGATGATTAATTCAGAACAA 441
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  692 AGTGGGCAAAATCTCTGAGGCAATTCACAA 722
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  440 ACTGGGCAAGATTTTCGATGAGATTCATAA 410
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 3
BE036541
LOCUS      MP01807 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION      antiviral protein, mRNA sequence.
ACCESSION      BE036541
VERSION        BE036541.1 GI:8331550
KEYWORDS       EST.
SOURCE         common iceplant.
ORGANISM       Mesembryanthemum crystallinum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE      1 (bases 1 to 1033)
AUTHORS        Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea
               , H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C.,
               Scara, G., Wheeler, M. and Zepeda, G.R.
               Functional Genomics of Plant Stress Tolerance
               Unpublished (2000)
               Contact: Michalowski, C.B.
               University of Arizona
               Bio Sciences West room 513, Tucson, AZ 85721, USA
               Tel: 520-621-7982
               Fax: 520-621-1697
               Email: cbm@u.arizona.edu
               An open reading frame exists.
               Location/Qualifiers
                 1..1033
                   /organism="Mesembryanthemum crystallinum"
                   /db_xref="taxon:3544"
                   /clone_lib="MP"
                   /tissue_type="apical meristem and leaf primordia"
                   /dev_stage="6 weeks"
                   /note="3 d 500mM NaCl"
BASE COUNT      273 a  206 c  260 g  34 others
ORIGIN

```

```

Query Match      9.2%  Score 87;  DB 10;  Length 993;
Best Local Similarity 60.1%  Pred. No. 7.8e-12;
Matches 163;  Conservative 0;  Mismatches 105;  Indels 3;  Gaps 1;

Oy  455 AGAAGCAGAGTAAACTCAAGAAATCAAGTCCCAATTCGAATTCGAAGTGC 514
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  680 AGAAGCTGCGGTCAAGCAGAAACAGATATTGACGTTGGGGCTTCTTAATATACATTTG 621
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  515 ACATTGCAAAATCTCTGGAGTTCATTCATTCCTCTGAAACAGTGGGCTTTTTCCTAC 574
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  620 CCATCGAGTCAATTTATGTTAAACAAACAGATCGATGGAAACATCGAGGCCAAATTCCTAC 562
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  575 TGTAGTCCATCTCAAGTTCAGAGCAGCGGATTCAGTCAAGTACATACAGAACCAAGT 632
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  561 TGATGTCATCCAGATCGTTTCAGAGCAGCAGGTTCCATATATCGACACTAAGTGC 502
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  633 -CAAGACTAATTTTAATAGAGCATTCTACCTGATCCCAAGTAATTAATTTTACAGAGA 691
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  501 CGAAGTGGTCAATCGTTCTCAACCCGATCGAAGATGATTAATTCAGAACAA 442
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Oy  692 AGTGGGCAAAATCTCTGAGGCAATTCACAA 722
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  441 ACTGGGCAAGATTTTCGATGAGATTCATAA 411
      |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 2
BE035038/c
LOCUS      MM02A01 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION      antiviral protein, mRNA sequence.
ACCESSION      BE035038
VERSION        BE035038.1 GI:8330047
KEYWORDS       EST.
SOURCE         common iceplant.
ORGANISM       Mesembryanthemum crystallinum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE      1 (bases 1 to 816)
AUTHORS        Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea
               , H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C.,
               Scara, G., Wheeler, M. and Zepeda, G.R.
               Functional Genomics of Plant Stress Tolerance
               Unpublished (2000)
               Contact: Michalowski, C.B.
               University of Arizona
               Bio Sciences West room 513, Tucson, AZ 85721, USA
               Tel: 520-621-7982
               Fax: 520-621-1697
               Email: cbm@u.arizona.edu
               Location/Qualifiers
                 1..816
                   /organism="Mesembryanthemum crystallinum"
                   /db_xref="taxon:3544"
                   /clone_lib="MM"
                   /cell_type="epidermal bladder cells"
                   /dev_stage="12 weeks old"
                   /note="vector: Bluescript SK+; Site_1: EcoRI; Site_2: XhoI
                   ; Plants stressed 6 weeks in 500mM NaCl"
BASE COUNT      234 a  173 c  171 g  238 t
ORIGIN

```

```

Query Match      8.5%  Score 80.6;  DB 10;  Length 816;
Best Local Similarity 58.7%  Pred. No. 3.4e-10;

```

06/02/2003

44

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 01:08:52 : Search time 1673 Seconds
(without alignments)
9148.078 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

Sequence: 1 atgaagtgatgctgttagt.....atctattgaaggattctaa 945

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hcc.*

9: gb_est1.*

10: gb_est2.*

11: gb_hcc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vit.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	87	9.2	993	BE035039	BE035039 MM02A03 M
C 2	80.6	8.5	816	BE035038	BE035038 MM02A01 M
C 3	65.6	6.9	1033	BE036541	BE036541 MP01B07 M
C 4	55.4	5.9	1038	BE033546	BE033546 MF03A09 M
C 5	52.4	5.5	405	T24255	T24255 crs1345 lam
C 6	50.8	5.4	639	BE037217	BE037217 MP18B02 M

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	47.2	5.0	837	10	AW053634
8	46.6	4.9	489	10	BE130330
9	45.4	4.8	267	9	AA856221
10	44.6	4.7	1021	10	BE036639
11	43.6	4.6	919	17	CNS0296A
C 12	42.4	4.5	561	17	AO156308
C 13	42.4	4.5	1101	17	CNS0039C
C 14	40.8	4.3	1001	17	CNS007RE
15	40.4	4.3	557	10	AW230870
16	40.4	4.3	567	10	AO670952
17	40.4	4.3	579	13	RJ365833
18	40.4	4.3	635	10	AW323815
19	40.4	4.3	685	13	BG920190
C 20	40	4.2	700	13	BM634714
C 21	40	4.2	715	13	BM654071
C 22	40	4.2	895	17	CNS015AJ
23	39.6	4.2	444	14	K31564
24	39.6	4.2	870	17	CNS0187R
25	39.6	4.2	1204	17	CNS016E2
26	39.4	4.2	456	12	BG555640
C 27	39.4	4.2	913	17	CNS00C20
C 28	39.2	4.1	1101	17	CNS00R6C
C 29	39.2	4.1	1101	17	CNS0100X
C 30	39.2	4.1	1146	17	CNS021C2
31	39	4.1	359	10	AW237651
32	39	4.1	684	14	BM982928
C 33	39	4.1	1019	17	CNS006FW
34	38.8	4.1	587	10	BE533685
C 35	38.6	4.1	593	13	BM610967
C 36	38.6	4.1	721	13	BM574953
37	38.4	4.1	860	17	AZ538875
C 38	38.4	4.1	1101	17	CNS017DU
C 39	38.2	4.0	512	13	AW199192
C 40	38.2	4.0	512	13	B1451206
C 41	38.2	4.0	680	13	BJ078909
42	38.2	4.0	870	17	CNS060U22
43	38	4.0	608	13	RJ397293
44	37.8	4.0	447	9	AA964758
C 45	37.8	4.0	676	13	BM585966

ALIGNMENTS

RESULT 1
BE035039/c BE035039 993 bp mRNA linear EST 07-JUN-2000
LOCUS MM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION Antiviral protein, mRNA sequence.

ACCESSION BE035039
VERSION EST
KEYWORDS EST
SOURCE Common iceplant.

ORGANISM Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Alzooaceae; Mesembryanthemum.

REFERENCE J (bases 1 to 993)

AUTHORS

Bolner, H.J., Rorchert, C., Brazill, S., Brooks, J., Eaton, M., Furra, H., Kawasaki, S., McCollough, A., Michalowski, C.U., Palencia, C., Scara, G., Wheeler, M. and Zepeda, C.R.

Functional Genomics of Plant Stress Tolerance

Unpublished (2000)

Contact: Michalowski, C.B.

University of Arizona

Bio Sciences West Room 513, Tucson, AZ 85721, USA

Tel: 520-621-7982

Fax: 520-621-1697

Email: chm@u.arizona.edu

Insert Length: 1 Std Error: 0.00.

Location/Qualifiers

Source

/organism="Mesembryanthemum crystallinum"

241 GCAACCTTAAACCACTTACACTAATGCTGAGACGAAATAAATTAACCTTATACGTGATGGCTAT 300
241 GCAACCTTAAACCACTTACACTAATGCTGAGACGAAATAAATTAACCTTATACGTGATGGCTAT 300
301 TCTGATCCCTTCAATGCGAATAAGTGTGCTTACCATATATTTAATGATATTAACAAGCACC 360
301 TCTGATCCCTTCAATGCGAATAAGTGTGCTTACCATATATTTAATGATATTAACAAGCACC 360
361 GAACGCACTGATGGGAGAACTACTCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCC 420
361 GAACGCACTGATGGGAGAACTACTCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCC 420
421 ATTAACCTAATAGCTTATATCGACCATGGAAGAAAGCAAGTAACTCAAGAAAT 480
421 ATTAACCTAATAGCTTATATCGACCATGGAAGAAAGCAAGTAACTCAAGAAAT 480
481 CAAGTCCAAATGGGAATTCAAATACCTCAGCAGTCAATTCGAAATAATCTCTGAGTTGAT 540
481 CAAGTCCAAATGGGAATTCAAATACCTCAGCAGTCAATTCGAAATAATCTCTGAGTTGAT 540
541 TCATCCCTGTAATAACTAGAGCTTTTCTTCTACTGGTACCCAAATCTCTGAGTTGAT 600
541 TCATCCCTGTAATAACTAGAGCTTTTCTTCTACTGGTACCCAAATCTCTGAGTTGAT 600
601 GCAGCGGATTCAGTACATAGAGCAACCAAGTCAAGACTAATTTAATAGAGCTTCTAC 660
601 GCAGCGGATTCAGTACATAGAGCAACCAAGTCAAGACTAATTTAATAGAGCTTCTAC 660
661 CTGATCCCAAGCTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGCAATTCAC 720
661 CTGATCCCAAGCTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGCAATTCAC 720
721 AATGCCAAGAAATGGGCTTTTACCACCAACTTGAAGTGGATGCCAAGTACCAAG 780
721 AATGCCAAGAAATGGGCTTTTACCACCAACTTGAAGTGGATGCCAAGTACCAAG 780
781 TGGATAGTCTTAGAGTGGATGAATCAATCGTGATGCGCACTCTTAAAGTACGTTAAT 840
781 TGGATAGTCTTAGAGTGGATGAATCAATCGTGATGCGCACTCTTAAAGTACGTTAAT 840
841 GGAACCTGTGAGCACTTACCAAAATGCCATGTTCTCAAGTTAATTTCTACTTAT 900
841 GGAACCTGTGAGCACTTACCAAAATGCCATGTTCTCAAGTTAATTTCTACTTAT 900
901 TATAATATATGCTAATCTGTGATGCTATTTGAAGGATTCTAA 945
901 TATAATATATGCTAATCTGTGATGCTATTTGAAGGATTCTAA 945

Printed 11/17/2004
US-09-978-274A-3
: Sequence 3, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978.274A
: PRIOR FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 792
: TYPE: DNA
: ORGANISM: Phytolacca americana
: US-09-978-274A-3

Query Match 83.2% Score 786.4; DB 10; Length 792;
Best Local Similarity 99.9%; Pred. No. 3.4e-214;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 73 ATAAATACCATCAGCTTTGATGCTGAAATGCAACATTAACAAATATGCAATCTTTATG 132
DB 4 ATAAATACCATCAGCTTTGATGCTGAAATGCAACATTAACAAATATGCAACATCTTTATG 63
QY 133 GAATCTCTTCTGTAATCAAGCGAAAGATCCAAACTAATAATGCTATGGCAATCAATGCTA 192
DB 64 GAATCTCTTCTGTAATCAAGCGAAAGATCCAAACTAATAATGCTATGGCAATCAATGCTA 123
QY 193 CCGTATACCTAATTCGACGCTTAAGTACTTATTCGTTAAGCTCCAAAGTCCAAACTTAAA 252
DB 124 CCGTATACCTAATTCGACGCTTAAGTACTTATTCGTTAAGCTCCAAAGTCCAAACTTAAA 183
QY 253 ACCATTACACTAATGCTGAGAGCAATAAATCTTATAGCTGATGGGTATTTGATGCTTTC 312
DB 184 ACCATTACACTAATGCTGAGAGCAATAAATCTTATAGCTGATGGGTATTTGATGCTTTC 243
QY 313 AATGGCAATAAGTGTCTTTACCATATATTTAATGATATTACAGCACCGAAGCTCAAT 372
DB 244 AATGGCAATAAGTGTCTTTACCATATATTTAATGATATTACAGCACCGAAGCTCAAT 303
QY 373 GTGGACAATACCTTTTCTCAAGTTCTAGTCTCGGTGTTGCAATGTCCTAATTAAC 432
DB 304 GTGGACAATACCTTTTCTCAAGTTCTAGTCTCGGTGTTGCAATGTCCTAATTAAC 363
QY 433 AGCTTATATCCGACCATGCAAGAAAGCAAGTAACTCAAGAAATCAATCTCAATTTG 492
DB 364 AGCTTATATCCGACCATGCAAGAAAGCAAGTAACTCAAGAAATCAATCTCAATTTG 423
QY 493 GGAATTCAAATACCTCAGCAGTGCATTTGAAAATCTCTGGAGTTGATTCATTTCTGTA 552
DB 424 GGAATTCAAATACCTCAGCAGTGCATTTGAAAATCTCTGGAGTTGATTCATTTCTGTA 483
QY 553 AAAATCAGGCTTTTCTTCTAGTGTGCTTCAAGTCTTCAAGTCTTCAAGGAGCGGCTTC 612
DB 484 AAAATCAGGCTTTTCTTCTAGTGTGCTTCAAGTCTTCAAGTCTTCAAGGAGCGGCTTC 543
QY 613 AAGTACATAGCAACCACTCAAGACTAATTTTAAATAGAGCAATTTTACCTGATCTCAAA 672
DB 544 AAGTACATAGCAACCACTCAAGACTAATTTTAAATAGAGCAATTTTACCTGATCTCAAA 603
QY 673 GTAAATTAATTTGAGGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCAAGAT 732
DB 604 GTAAATTAATTTGAGGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCAAGAT 663
QY 733 GGGCTTTTACCCAAACCACTTGGATGCTAGTGGATGCAAGGTTACCAAGTGGATTTCT 792
DB 664 GGGCTTTTACCCAAACCACTTGGATGCTAGTGGATGCAAGGTTACCAAGTGGATTTCT 723
QY 793 AGAGTGGATGAATCAATCTGATGTCGACCTCTTAACTAGTCTTAACTAGAACTTCTAG 852
DB 724 AGAGTGGATGAATCAATCTGATGTCGACCTCTTAACTAGTCTTAACTAGAACTTCTAG 783
QY 853 ACAACTTA 860
DB 784 ACAACTTA 791

RESULT 3
US-09-978-274A-19
: Sequence 19, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978.274A

Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Alkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978-274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1375
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-30

Query Match 66.9% Score 632.4; DB 10; Length 1379;
Best Local Similarity 80.0% Pred. No. 4.3e-170;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

73 ATAAATACGATCAGCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 132
4 ATAAATACGATCAGCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 63
133 GAATCTCTTCGTAATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATGCTA 192
64 GAATCTCTTCGTAATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATGCTA 123
193 CCGTACTAATTCGACCCCTAAGTACTTATTGGTTAAGCTCCAAAGTGCAACCTTAA 252
124 CCGTACTAATTCGACCCCTAAGTACTTATTGGTTAAGCTCCAAAGTGCAACCTTAA 183
253 ACCATTACACTAATCTGAGAGGAATAACTTATACGTGATGGGCTATTCTGATCCCTTC 312
184 ACCATTACACTAATCTGAGAGGAATAACTTATACGTGATGGGCTATTCTGATCCCTTC 243
313 AATGGCAATTAAGTGTCTGATACCATATATTATGATATTACAGAGCGGCAACCTGAT 372
244 AATGGCAATTAAGTGTCTGATACCATATATTATGATATTACAGAGCGGCAACCTGAT 303
373 GTGAGNACTCTTCTGCTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
304 GTGAGNACTCTTCTGCTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
433 AGCTTATATCCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
364 AGCTTATATCCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
493 GGAATTCAAATATCTACGAGTGCATTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
424 GGAATTCAAATATCTACGAGTGCATTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
553 AAAAAGTGGGCTTTTCTTCTACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
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613 AAGTACATAGAGAACCAAGTCAAGACTAATTTTATAGAGACTTCTACCTGATCCCAAA 672
544 AAGTACATAGAGAACCAAGTCAAGACTAATTTTATAGAGACTTCTACCTGATCCCAAA 603
673 GTAATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 732
604 GTAATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 663
733 GGGGCTTTTACCAAAACCACTTGAAGTGTGGATGCGCAAAAGGTACCAAGTGGATAGTTCT 792
664 GGGGCTTTTACCAAAACCACTTGAAGTGTGGATGCGCAAAAGGTACCAAGTGGATAGTTCT 723
793 AGAGTGCATGAATCAATCTGATGCTGATGCGCAAAAGGTACCAAGTGGATAGTTCT 835
724 AGAGTGCATGAATCAATCTGATGCTGATGCGCAAAAGGTACCAAGTGGATAGTTCT 766

Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Alkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978-274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1375
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-30

Query Match 66.9% Score 632.4; DB 10; Length 1379;
Best Local Similarity 80.0% Pred. No. 4.3e-170;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

3 GAAGCTGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 62
221 GAAGATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 280
63 AACTTGTGCTAATTAATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 122
281 AACTTGTGCTAATTAATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 340
123 CACCTTTATGGAATCTCTGCTAATCAAGCGAAGATCCAAAGTGCAACCTTAA 182
341 CACCTTTATGGAATCTCTGCTAATCAAGCGAAGATCCAAAGTGCAACCTTAA 400
183 ACCAATGCTACCTGATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 242
401 ACCAATGCTACCTGATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 460
243 AACCTTAAACCATTAATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 302
461 AAATFAAAACCATTAATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 520
303 TGATCCCTTCAATGCGCAATTAAGTGTCTTACCATATATTTAATGATATTAACAAATATGCC 362
521 TGATCCCTTCAATGCGCAATTAAGTGTCTTACCATATATTTAATGATATTAACAAATATGCC 580
363 AGGCACTGATGCGGAGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 422
581 AGGCACTGATGCGGAGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 640
423 TAAGTACATGCTTTATATGCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 482
641 AAACCTTTGATGCGGAGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 700
483 AGTCCAAATGGCAATTAATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 542
701 GGTCCAACTGGCAATTAATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 760
543 ATTCCCTTAAACCTGAGGCTTTTCTGCTGATGCGCAAAAGGTACCAAGTGGATAGTTCT 602
761 ATTCCCTTAAACCTGAGGCTTTTCTGCTGATGCGCAAAAGGTACCAAGTGGATAGTTCT 820
603 AGGCGGATCAAGTACATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 662
821 AGCAAGATTTCAAGTACATGATGCTTTGATGCTGGAATGCCACCATTAACAAATATGCC 880
663 TGATCCCAAGTACATTAATTTGCGAGGAGAGAGTGGGCAAAAGGTACCAAGTGGATAGTTCT 722
881 TAATCCCAAGTACATTAATTTGCGAGGAGAGAGTGGGCAAAAGGTACCAAGTGGATAGTTCT 940
723 TGCCAAAGATGGGCTTTTCTGCTGATGCGCAAAAGGTACCAAGTGGATAGTTCT 782

941 TCCCAAGATGGAGTTTACCCAAACCTCTCGAGCTAGTGGATGCCAGTGGTCCCAAGTG 1000
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843 AACCTCTCAGACAACCT---ACCAAAATGCCATGTTCTCTCAAGCTTATATTTCTACTTA 899
1061 GAGCTGTGAGACAACCTTAAACCAAAATGCCATGTTCTCTCAAGCTTATATTTCTACTTA 1120
900 TTATAATTATATCTCTAATCTTTGGTGTGATCTATTGGAAGGATTTCTAA 945
1121 TTATAATTATATCTCTAATCTTTGGTGTGATCTATTGGAAGGATTTCTAA 1166

RESULT 5
US-09-978-274A-31; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1

; GENERAL INFORMATION:

; APPLICANT: Thomas, Christopher

; APPLICANT: McPherson, Michael

; APPLICANT: Atkinson, Howard

; APPLICANT: Neelam, Anil

; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM

; FILE REFERENCE: 9341-028

; CURRENT APPLICATION NUMBER: US/09/978,274A

; PRIOR FILING DATE: 2001-10-15

; PRIOR FILING DATE: 2000-10-14

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 1368

; TYPE: DNA

; ORGANISM: Phytolacca americana

US-09-978-274A-31

Query Match 66.6%; Score 629.2; DB 10; Length 1368;

Best Local Similarity 79.8%; Pred. No. 3.5e-169;

Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

3 GAAGTGTGCTGTGTAGTGTGTGCTGACGTTAATAGCTGGCTCATTGCTGCACCACTTC 62
221 GAAGTGAAGTCAATGCTGTGTGCTGACATATCAATATGCTCATCTTGTGCACCACTTC 280
63 AACTTGTGCCATAAATACGATCACTTGTGCTGGAATGCCACATTAACAATATGC 122
281 AACTTGGGCTGTGAATACAAATCATCTCAATGTTGGAGTACCACTTAGCAAAATAGC 340
123 CACCTTTATGGAATCTCTTCGTAATCAAGCGAAGATCCAAACTAAATGCTATGGCAT 182
341 CACTTTTCGGAATGATCTCTGTAATGAACGGAAGATCCAACTTAAATGCTATGGAT 400
183 ACCAATGCTACTGATCACTAATTCGACCCCTAAGTACTTATGGTTAAGCTCCAAAGTGC 242
401 ACCAATGCTGCCAATACAAATACAAATCAAAATCCAAAGCACGTTGGTTGAGCTCAAGTTC 460
243 AAACCTAAACCACTTACACTAATGCTGAGACGAAATACCTTATACGTGATGGCTATTC 302
461 AAATAAACAACCATCACACATATGCTGAGCGAACAATTTGTATGATGGTGGTTATTC 520
303 TGATCCCTTCAATGCCAATAGCTGCTGTGTTACCATATATTTAATGATATTTACAGCACCA 362
521 TGATCCCTTGAACCAATAAATGCTGTGTTACCATATCTTTAATGATCTCTAGGTACTGA 580
363 AGCGACTGATGGAGATACCTTTTGTCTAGTCTTCTAGTCTGCTGTGCAATGCTCAT 422
581 AGCGCAAGATGTAGAGACTACTCTTTGCCAAATGCCAATCTCTGTTAGTAAACAT 640
423 TAACATCAATAGCTTATATCCGACCATCGAAAGAACAGCAAGTAACTCAAGAAATCA 482

640 GATGCCAATGGGTATCAGCCAGATCTTAAAGCTATTTCCTAGAGAAAATTTGGCAGCT. 699
703 ATCTCTGAGCAATTCACAATGCCAAGATGGGGCTTTACCCAAACCACTTTGAGCTAGTG 762
700 GTTCTAAGGCTATTCGCAAAAGTTGGCAACCTCCCGGTGATAGTACTGTTACTTTACCTGGA 759
763 GATGCCAAGGTACCAAGTGGATAGTCTTCTAGAGTGGATGAATCAATCGTGTGGA 822
760 GACCTAAAGATGACAATAATAAACCTTGGACTAGGGCACCACCAAGCACCCTTAAGAAC 819
823 CTCTCTAAGTACGTTAAATGGAACCTCTCAGACAACCTTACCAAAATGCCATGTTCTCTCAA 882
820 GACATATGGCACTCCTCAACCCACCTTACTTGCAGAGTTAAAGTTCCATGTTCCCTGAA 879
883 GTTATAATTTCTACTATTATATAATATATATGCTTAATCTTGGTGA 926
880 ATTATGCTCTATTATATAGGACTAGTATTAGTAACCTTGGTGA 923

RESULT 9

US-09-861-257-37
Sequence 37, Application US/09861257

Publication No. US20030040496A1

GENERAL INFORMATION:

APPLICANT: Chandier, Lois Ann

APPLICANT: Sosnowski, Barbara A.

APPLICANT: Baird, J. Andrew

APPLICANT: Pierce, Glenn

TITLE OF INVENTION: TREATMENT OF TUMORS USING

TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESS: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/861,257

FILING DATE: 17-MAY-2001

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Christiansen Ph.D., William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 760100.423C1

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 804 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..804

FEATURE:

NAME/KEY: misc-feature

LOCATION: 1..804

OTHER INFORMATION: /note= "Nucleotide sequence

OTHER INFORMATION: corresponding to the clone M13 mp18-G7"

FEATURE:

NAME/KEY: mat-peptide

LOCATION: 46..804

OTHER INFORMATION: /product= "Saporin"

US-09-861-257-37

Query Match

Best Local Similarity 9.4%; Score 88.4; DB 9; Length 804;

Matches 376; Conservative 49.3%; Pred. No. 6.1e-15;

Mismatches 0; Mismatches 371; Indels 15; Gaps 5;

QY 47 TTGCTGACCAACTTCAACTTGTGCTAATAATAGATCACCTTTGTGCTGGAATGCA 106
DB 20 TTTCAGCTTGGCAACCACTGATCGGTCACATCAATCACATTACATCTAATAATGCA 79
QY 107 CCATTAAACAAATATGCCACCTTTATGCAATCTCTTGGTAATCAAGCGAAGATGCAAAAC 166
DB 80 CCGGGGTCAATACATCATCTTTTGTGATTAATTCGAAACAGCTAAGATGCAAAAC 139
QY 167 TAAATGCTATGGATACCAATGC---TACCTGATACTAATTCGACCCCTTAAGATGAT 223
DB 140 TCAATACGCTGGTACCGACATAGCCGTGATAGCCCACTTCTTAAGAAATATCTTA 199
QY 224 TGGTTAAGCTCCCAAGGTGCAAACTTAAACCATTAACATTAAGTGTGAGAGCAATTA 283
DB 200 GAATTAATTTCCAAAGTTC---CGAGGACGGTCTCCTCTGGCCTAATAAGATTA 256
QY 284 TATAGCTGATGGGTATTTCTGATCCCTTCAATGCAATAAGTGTCTGTATCATATATTA 343
DB 257 TGTATGTTGGTCCGCTATCTTCCATGATACACGAATGTTAATCGGCGCATATTTCTCA 316
QY 344 ATGATATTACAGCACCACGACGACTGATGAGAGATATCTTTTCTCAAGTTTCTACT 403
DB 317 GATCAGAAATTAATTTCCGCGGAGTTAAACCGGCTTTTCCAGAGAGGCGCAATTC 376
QY 404 CTGCTGTTGCAATGTCATTAACATACATATATATCCGACCATGSAAGAAAGACAG 463
DB 377 AGAAGCTTTAGATACACACAGATTAATAGTCGATCGAAGAAAGATCCCGGATAC 436
QY 464 AAGTA---AATCAAGAAATCAAGTCCAAATTTGGAATTAATCAATCACTCAGCAGTCA 520
DB 437 AGGAGATATAATCAAGAAAGAACTCGGTTGGGATCGGCTTACTTTGAGTCTGATGG 496
QY 521 GAAATCTCTGGAGTGTGATTCCTCTGTAAACACTGAGGCTTTTCTTCTACTGTAG 580
DB 497 AGCAGTGAACAAGA---AGGACGCTGTGTTAAACGAAGCTAGATTCCTTCTTATGG 553
QY 581 CCATCCAAATGTTTCAAGAGCGGCGGATTCAGATACATAGAGAAACAATTAAGACTA 640
DB 554 CTATTCAGATCAAGCTCGAGGCGGACGATTTAGGTACATACAAACTTCTTAATCA 613
QY 641 ATTTTAATAGAGCATTTTACCTGATCCCAAGTAATTAATTTGGAGAGCAAGTGAAGCA 700
DB 614 ACTTTCGCAACAATTTCACTCGGAAACAAAGTCAATTTCAAGTTAAATGGAAGA 673
QY 701 AAATCTCTGAGGCAATTCAG---AATGCAAGATGGGCTTTACCCCAACCACTTCAGC 757
DB 674 AATTTCTACGGCAATATACGGGATGCAAAACGGGCTTTTAATTAAGATTAATGATT 733
QY 758 TAGTGGATGCCAAAGTACCAAGTGTAGTCTTTAGAGTGG 799
DB 734 TCGGCTTTGGAAAGTGAAGCAGGCTGAAGGACTTCCAAATCG 775

RESULT 10

US-09-861-257-38

Sequence 38, Application US/09861257

Publication No. US20030040496A1

GENERAL INFORMATION:

APPLICANT: Chandier, Lois Ann

APPLICANT: Sosnowski, Barbara A.

APPLICANT: Baird, J. Andrew

APPLICANT: Pierce, Glenn

TITLE OF INVENTION: TREATMENT OF TUMORS USING

TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

us-09-978-274a-1.rnbp

Mon Jun 2 10:54:58 2003

ADDRESSES: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/861,257
FILING DATE: 17-MAY-2001

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100.423C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804

OTHER INFORMATION: /note= "Nucleotide sequence
corresponding to the clone M13 mpl8-G9"
OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"

US-09-861-257-38
Query Match 9.4%; Score 88.4; DB 9; Length 804;
Best Local Similarity 49.3%; Pred. No. 6.1e-15;
Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

47 TTGCTGACCACTTCAACTGTGGCCATAAATACGATCACCTTTGATGCTGGAAATGCCA 106
20 TTTCAGCTGGGACAACTGATGCGGTACATCAATCATCATAGATTAGTAATCCGA 79
107 CCATTAACAATAATGCCACCTTTATGATCTCTTGTATCAAGCGAAGATCCAAAC 166
80 CCGCGGTCAATCACTCTTTTGTGATAAATCCGAAACAACTGAAGATCCAAAC 139
167 TAAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 223
140 TGAATACGGTGTGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 199
224 TGGTAACTCCAGGTGCAAACTTAAATCAATCAATCAATCAATCAATCAATCAATCA 283
200 GAATTAATTTCCAAAGTTC---CCGAGGAGCGGTCTCACTTGGCTTAAACCGCATAC 256
284 TATACGTATGGGTATCTGATCCCTTCAATGCAATAAGTCTGTTACCATATATTA 343
257 TGTATGTCGCGTATCTTGCATATGATAACCAAGATGTTAATCGGGCATATTA 316
344 ATGATATTACAGCAACCAAGCGCTGATGCTGAGAGATCTCTTTGCTCAAGTTCTAGT 403
317 CATCAGAAATTAATCTCCCGCGAGTTAAACCGGCTTTTCCAGAGCGCACTGCAATC 376
404 CTCGCTGTCATGTCATTAATCACTACATAGCTTATATCCGACCATGGAAGAAGCAG 463

Db 377 AGAAGCTTTAGATACACAGAGATTATCAGTCGATTGAAAGAAATGCCGATACAC 436
Qy 464 AAGTAACTCA---AGAAATCAATGTCGAATTTGGGAATTCAAATCACTCAGCAGTCA 520
Db 437 AAGGAGATCAAAAGTAGAAAGAAAGTGGGTTGGGATTTGCTTCTTCAAGCTGATGG 496
Qy 521 GAAATATCTCTGAGTTCATTCATTCCTCTGTAATAAAGTGAAGGCTTTTCTTTTAT 580
Db 497 AAGCAGTGAACAAGA---AGGCAGCTGTGCTTAAGACGCAAGCTAGATTCCTTCT 553
Qy 581 CCATCCAAATGTTTTCAGAGCGGCGGATTTCAAGTACATAGAGAACCAAGTCAACACT 640
Db 554 CTATTCAGATGACGCGCTGAGCGCGGATTTAGGTACATACAAAACCTTGGTAATCA 613
Qy 641 ATTTAATAGACCATTTCTACCTGATCCCAAGTAAATTAATTTGGAGGAGAAATGAG 700
Db 614 ACTTCCCAACAAGTTTCAACTCCGAAACAAGATGATTCAGTTTGAAGTGAAGAA 673
Qy 701 AATCTCTGAGCAATTCAC---AATGCCAAGAAATGGGCTTTTACCCAAACACCTTCA 757
Db 674 AATTTCTAGCGCAATATACGGGATGCCCAAAACGCGGTGTTTAATAAGATTTATCA 733
Qy 758 TAGTGGATGCCAAAGCTTACCAATGATGATCTTCTTACAGTGG 799
Db 734 TCGGTTTGGAAAGTGAAGCGAGTCAAGGACTTGCAAATGG 775

RESULT 11
US-09-792-793A-66
Sequence 66, Application US/09792793A
Patent No. US20020168170A1

GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-6010
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 765

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
OTHER INFORMATION: Methionine-Saporin fusion protein

NAME/KEY: CDS
LOCATION: (21)..(765)
US-09-792-793A-66

Query Match 8.9%; Score 84; DB 9; Length 765;
Best Local Similarity 47.3%; Pred. No. 1.1e-13;
Matches 320; Conservative 0; Mismatches 350; Indels 6; Gaps 2;

Qy 74 TAAATACGATCACTTTGATGCTGGAATGCCACCATTAACAAATATGCCACTTATG 133
Db 74 TAAATACGATCACTTTGATGCTGGAATGCCACCATTAACAAATATGCCACTTATG 64
134 AATCTCTGATTAACAGCGAAGATCCAAACTTAAATGCTATGCTATGCTATGCTATG 193
Qy 65 ATAAGATTCGTACACAGCTAAGATCCGAATCTGAATACGCTGCTATGATTTGCG 124
Db 194 CTGATACCTAATTCGACCCCTTAAGTACTTATTTGTTAGCTCCCAAGTGAACAA 253
Qy 125 TCATCGGTCCCGCGCAAGCAAGAAAGTTCTCGGCATTAATCTTCAAGCTGCTAT 184
Db 254 CCATTACTAATGCTCAGACGAATAAATCTATACGTGATGGGCTATTCGATGCTTCA 313
Qy 185 CTGTTCTCTGGGGCTGAAGCGGCAATCACTGATGTTGCTGCTATCTGCGATGATA 244
Db 314 ATGCAATTAAGTCTGCT---TACCATATATTTAATGATATTATACAGCACTGAC 370

245 ATACGACCTGAACCGCCCTACTACTTTCGTAGCGAGATTACGAGCGGGAATCCACTG 304
371 ATGTGGAGAATACTCTTTGCTCAAGTCTTAGTCTCGTGTTCGCAATGTCCATTAACTACA 430
305 CTCTGTTCGCGGAGCGACCACTGCAACACCAAAAGACACTGCAATATACGGAAGATTACC 364
431 ATAGCTTATATCCGACCATGGAAGAAGACAGAGTAACATCAAGATCAAGTCCCAT 490
365 ATCCATCAGAGAAGCGCGAGATCAACCGGCGGATCAATCCCGCAAGAACTGGGTC 424
491 TGGGAATTCAAATACTACAGCACTGACATTTGGAATAATCTCTGGAGTTGATTCTCCCTG 550
425 TGGGTATTGATCTGTGACGACGAGCATGGAAGCGGTCAACAAA---AAGCTCGGGTG 481
551 TAAAACTGAGCGCTTTTCTTCTACTGAGTGCATCAAAATGTTTCAGAGCGAGCGCAT 610
482 TTAAGACGAAAGCGCGCTTCTGCTGATCGCCATTGATGCGGACGAGAGCGCGCGGT 541
611 TCAAGTACATACAGAACCAAGTCAAGCACTAATTTTAATAGAGCACTTCTACCTGATCCA 670
542 TCGGTACATTCAGAACCTGGTGTCAAAACTTCCCGAACAGTTCAATTCGGAATA 601
671 AAGTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAATGCGCAAGA 730
602 AAGTCATTGATCGAGGTTAATTTGGAATAAATTTCCACCGCCATTATGTTGTCGCGA 661
731 ATGGGCGCTTACCCAA 746
662 AGAACGGTGTTCCTCAA 677

RESULT 12

US-09-792-793A-60
Sequence 60, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coghins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 984
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
NAME/KEY: CDS
LOCATION: (1)...(984)
US-09-792-793A-60

Query Match 8.9% Score 84: DB 9: Length 984:
Best Local Similarity 47.3% Pred. No. 1.2e-13:
Matches 320: Conservative 0: Mismatches 350: Indels 6: Gaps 2:
74 TAAATACCATCACTCTTTCATGCTGGAATATGCCACCAATTAACAAATATGCCACCTTTATGG 133
224 TTACTAGTATTACCTCGACCTGGTGTCAATCCGACCGCGGCAATATACCACTTCGTGG 283
134 AATCTCTTCTGTAATCAGCGAAGATCCAAACTAAATGCTATGCGATPACCAATGCTAC 193
284 ATAAGATCGTAACACGCTAAAGATCCGAATCTGAATACGCTGCTACTGATATTCGG 343
194 CTGATCACTAATTCGACCCCTTAGTACTTATTGGTTAGCTTCCAAAGTCCGAACCTTAARA 253
344 TCATCGTCCGCGCAAGAAAGTTCTCGGCAATTAATTTCAAGCTCCCGTGGCA 403

254 CCAATTACACTAATGCTGAGAGCAATAAATTATAGGTGATGGCTATTCTCAATCCCTTCA 313
404 CTGTTTCTCTGGGCTTGAAGCGGATACACCTGTATGTTGTTCCCTATCTGCTGCGATGATA 463
314 ATGSCAATAAGTGTCTGCT---TACCATATATTAATGATATTACAAGACCAATGCACTG 370
464 ATACGAACTGAAACCGCGCTACTACTTTCGTAGGAGATTACGAGCGCGGAATCCACTG 523
371 ATGTGGAGAACTACTCTTTGCTCAAGTCTTAGTCTCTGCTGTTGCAATGTCCATTAACTACA 430
524 CTCCTCTCCGAGGCGACCACTGCAACACCAAAAGCACTGCAATATACGGAATATACC 583
431 ATAGCTTATATCCGACCATGGAAGAAGACAGAGTAACATCAAGATCAAGATCAATTCAT 490
584 ATCCATCGAAGAACCGCGAGATCAACCGGCGATCAATCCCGCAAGAACCTGCTC 643
491 TGGGAATTCAAATACTACAGCACTGACATTTGGAATAATCTCTGGAGTTGATTCTCACTG 550
644 TGGGTATTGATCTGTGACGACGACCATGGAAGCGGTCAACAAA---AAGCTCGGGTG 700
551 TAAAACTGAGCGCTTTTCTTCTACTGAGTGCATCAAAATGTTTCAGAGCGAGCGCAT 610
701 TAAAGACGAAAGCGCGCTTCTGCTGATCGCCATTGATGCGGACGAGAGCTGCTGCT 760
611 TCAAGTACATACAGAACCAAGTCAAGCACTAATTTTAATAGAGCACTTCTACCTGATCCA 670
761 TCGGTACATTCAGAACCTGGTGTCAAAACTTCCCGAACAGTTCAATTTCCGAATA 820
671 AAGTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAATGCGCAAGA 730
821 AAGTCATTGATCGAGGTTAATTTGGAATAAATTTCCACCGCCATTATGTTGTCGCAAGA 880
731 ATGGGCGCTTACCCAA 746
881 AGAACGGTGTTCCTCAA 896

RESULT 13

US-09-792-793A-63
Sequence 63, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coghins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 993
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(993)
OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine
OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
US-09-792-793A-63

Query Match 8.9% Score 84: DB 9: Length 993:
Best Local Similarity 47.3% Pred. No. 1.2e-13:
Matches 320: Conservative 0: Mismatches 350: Indels 6: Gaps 2:
74 TAAATACCATCACTCTTTCATGCTGGAATATGCCACCAATTAACAAATATGCCACCTTTATGG 133
233 TTACTAGTATTACCTCGACCTGGTGTCAATCCGACCGCGGCAATATACCACTTCGTGG 292
134 AATCTCTTCTGTAATCAGCGAAGATCCAAACTAAATGCTATGCGATPACCAATGCTAC 193
293 ATAAGATCGTAACACGCTAAAGATCCGAATCTGAATACGCTGCTGCTGCTGCTGCTGCTG 352

239 TTACTAGTATTACCTGGACCTGGTCAATCCGACCGCGCAATATATACAGTTCCTGG 298
134 AATCTCTTCTATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATCTTAC 193
299 ATAAGATTCCTAACAAAGTAAAGATCCCAATCTGAATACGCTGCTACTGATATTCG 358
194 CTGATCTAATTCGACCTTACGCTTATTTAGCTTCCAGCTGCAAACTTAAATA 253
359 TCATCGCTCCCGCGAGCAAAAGAACTTCTCGCATTAACCTTCAAAAGCTTCTGGCA 418
254 CCATTACACTAATCTCGAGCAAGAAATACCTTATACGTGATGGCTATTCGATCTTCA 313
419 CTCTTCTCTGGGCTTGAAGCGGATTAACCTGATGTTGCTCTATCTCTGATGATATA 478
314 ATGCGCAATAAGTCTGT---TACCATATATTTAATGATATTACAAAGCAAGAGACTG 370
479 ATGCAAGCTGAACCGGCTTACTTCTGCTAGCGAGATTACGAGCGGAAATTCAGCTG 538
371 ATGTGGAGAACTCTTTTCTGCTAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
539 CTCTGTTCCGAGCGGCACTTCCAAAGCAAAAGCACTGGAATATACGTAAGATTACC 598
431 ATAGCTTATATTCGACCATGAAAGAAAGCAAGTAAGTCAAGAAATCAACTTCAAT 490
599 AGTCATCGAGCAAGCAAGCGGAGATCACCGAGGCGGATCAATCCCGCAAGCAATCTG 658
491 TGGGAATCAATCTACGAGTACATGGAATAATCTCTGGAGTTGATTCATTCCTGCTG 550
653 TGGTATTGCTGCTGAGCAGCAGCATGGAAGCGGTCAACAAA---AAGCTCGCGTGG 709
551 TAAAGCTGAGCTTTTCTTCTGCTAGCCATCCAAATGTTTCAAGAGCGGCGGAT 610
710 TTAAGAGCAAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
611 TCAAGTACATAGCAAGCAAGTCAAGACTTAATTTAATAGAGCATCTTACCCTGATCCA 670
770 TCGCTACATTCAGAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
671 AAGTAATTAATTTGGAGGAGAGTGGGGCAAAATCTCTGAGCAATTCACATGCGCAAG 730
830 AAGTCATTCAGTTCGAGGTTAATTTGGAAGAAATTTCCACCGCCCTTTATGTTGAGCG 889
731 ATGGGCTTTACCCAA 746
890 AGAAGCGTGTTTTCAA 905

RESULT 14
US-09-792-793A-54
; Sequence 54, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine- toxin fusion protein MCP1-AM-SAPORIN
; OTHER INFORMATION: toxin fusion protein MCP1-AM-SAPORIN
; US-09-792-793A-54

Query Match 8.9% Score 84; DB 9; Length 999;
Best Local Similarity 47.3%; Pred. No. 1.3e-13;
Matches 320; Conservative 0; Mismatches 350; Indels 6; Gaps 2;
74 TAAATACGATCCTTTGATGCTGGAATGCCACCATTAACAATATGACCTTTATCG 133

239 TTACTAGTATTACCTGGACCTGGTCAATCCGACCGCGCAATATATACAGTTCCTGG 298
134 AATCTCTTCTATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATCTTAC 193
299 ATAAGATTCCTAACAAAGTAAAGATCCCAATCTGAATACGCTGCTACTGATATTCG 358
194 CTGATCTAATTCGACCTTACGCTTATTTAGCTTCCAGCTGCAAACTTAAATA 253
359 TCATCGCTCCCGCGAGCAAAAGAACTTCTCGCATTAACCTTCAAAAGCTTCTGGCA 418
254 CCATTACACTAATCTCGAGCAAGAAATACCTTATACGTGATGGCTATTCGATCTTCA 313
419 CTCTTCTCTGGGCTTGAAGCGGATTAACCTGATGTTGCTCTATCTCTGATGATATA 478
314 ATGCGCAATAAGTCTGT---TACCATATATTTAATGATATTACAAAGCAAGAGACTG 370
479 ATGCAAGCTGAACCGGCTTACTTCTGCTAGCGAGATTACGAGCGGAAATTCAGCTG 538
371 ATGTGGAGAACTCTTTTCTGCTAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
539 CTCTGTTCCGAGCGGCACTTCCAAAGCAAAAGCACTGGAATATACGTAAGATTACC 598
431 ATAGCTTATATTCGACCATGAAAGAAAGCAAGTAAGTCAAGAAATCAACTTCAAT 490
599 AGTCATCGAGCAAGCAAGCGGAGATCACCGAGGCGGATCAATCCCGCAAGCAATCTG 658
491 TGGGAATCAATCTACGAGTACATGGAATAATCTCTGGAGTTGATTCATTCCTGCTG 550
653 TGGTATTGCTGCTGAGCAGCAGCATGGAAGCGGTCAACAAA---AAGCTCGCGTGG 709
551 TAAAGCTGAGCTTTTCTTCTGCTAGCCATCCAAATGTTTCAAGAGCGGCGGAT 610
710 TTAAGAGCAAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
611 TCAAGTACATAGCAAGCAAGTCAAGACTTAATTTAATAGAGCATCTTACCCTGATCCA 670
770 TCGCTACATTCAGAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
671 AAGTAATTAATTTGGAGGAGAGTGGGGCAAAATCTCTGAGCAATTCACATGCGCAAG 730
830 AAGTCATTCAGTTCGAGGTTAATTTGGAAGAAATTTCCACCGCCCTTTATGTTGAGCG 889
731 ATGGGCTTTACCCAA 746
890 AGAAGCGTGTTTTCAA 911

RESULT 15
US-09-792-793A-57
; Sequence 57, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine- toxin fusion protein MCP3-AM-SAPORIN
; OTHER INFORMATION: toxin fusion protein MCP3-AM-SAPORIN
; US-09-792-793A-57

239 TTACTAGTATTACCTGGACCTGGTCAATCCGACCGCGCAATATATACAGTTCCTGG 298
134 AATCTCTTCTATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATCTTAC 193
299 ATAAGATTCCTAACAAAGTAAAGATCCCAATCTGAATACGCTGCTACTGATATTCG 358
194 CTGATCTAATTCGACCTTACGCTTATTTAGCTTCCAGCTGCAAACTTAAATA 253
359 TCATCGCTCCCGCGAGCAAAAGAACTTCTCGCATTAACCTTCAAAAGCTTCTGGCA 418
254 CCATTACACTAATCTCGAGCAAGAAATACCTTATACGTGATGGCTATTCGATCTTCA 313
419 CTCTTCTCTGGGCTTGAAGCGGATTAACCTGATGTTGCTCTATCTCTGATGATATA 478
314 ATGCGCAATAAGTCTGT---TACCATATATTTAATGATATTACAAAGCAAGAGACTG 370
479 ATGCAAGCTGAACCGGCTTACTTCTGCTAGCGAGATTACGAGCGGAAATTCAGCTG 538
371 ATGTGGAGAACTCTTTTCTGCTAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
539 CTCTGTTCCGAGCGGCACTTCCAAAGCAAAAGCACTGGAATATACGTAAGATTACC 598
431 ATAGCTTATATTCGACCATGAAAGAAAGCAAGTAAGTCAAGAAATCAACTTCAAT 490
599 AGTCATCGAGCAAGCAAGCGGAGATCACCGAGGCGGATCAATCCCGCAAGCAATCTG 658
491 TGGGAATCAATCTACGAGTACATGGAATAATCTCTGGAGTTGATTCATTCCTGCTG 550
653 TGGTATTGCTGCTGAGCAGCAGCATGGAAGCGGTCAACAAA---AAGCTCGCGTGG 709
551 TAAAGCTGAGCTTTTCTTCTGCTAGCCATCCAAATGTTTCAAGAGCGGCGGAT 610
716 TTAAGAGCAAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
611 TCAAGTACATAGCAAGCAAGTCAAGACTTAATTTAATAGAGCATCTTACCCTGATCCA 670
776 TCGCTACATTCAGAACCTTGTGCTATCAAAAGCTTCCCGCAAGCTTCAATTCGCAAGA 835
671 AAGTAATTAATTTGGAGGAGAGTGGGGCAAAATCTCTGAGCAATTCACATGCGCAAG 730
836 AAGTCATTCAGTTCGAGGTTAATTTGGAAGAAATTTCCACCGCCCTTTATGTTGAGCG 895
731 ATGGGCTTTACCCAA 746
896 AGAAGCGTGTTTTCAA 911

01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (cRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain).
Ricin communis (Castor bean).
Ricin communis (Castor bean).
Lukarota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eumetazoa; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
NCBI_TaxID=3988;
[1]
SEQUENCE FROM N.A.
MEDLINE=86059449; PubMed=2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.:
"The primary sequence of Ricinus communis agglutinin. Comparison with ricin."
J. Biol. Chem. 260:15682-15686(1985).
[2]
SEQUENCE OF 303-564.
TISSUE=Seed.
C Araki T., Yoshioka Y., Funatsu G.:
"The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds.";
Biochim. Biophys. Acta 872:277-285(1986).
[3]
SEQUENCE OF 303-337.
MEDLINE=80178723; PubMed=6768555;
Lin T.T.-S., Li S.S.-L.:
"Purification and physicochemical properties of ricins and agglutinins from Ricinus communis."
Eur. J. Biochem. 105:453-459(1980).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.

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EMBL: M12089; AAA33869.1; -;
EMBL: S40368; AAB22584.1; -;
PIR: A24261; RLCSAG.
HSP: P02879; IIRK6.
GlycoSuiteDB: P06750; -;
InterPro: IPR001574; RIP.
InterPro: IPR000772; Ricin_B_lectin.
Pfam: PF00161; RIP; 1.
Pfam: PF00652; Ricin_B_lectin; 6.
PRINTS: P000396; SHIGARICIN.
SMART: SM00458; RICIN; 2.
PROSITE: PS00231; RICIN_B_LECTIN; 2.
PROSITE: PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
SIGNAL 1 24
CHAIN 25 290
AGGLUTININ A CHAIN.
PROPEP 291 302
LINKER PEPTIDE.
CHAIN 303 564
AGGLUTININ B CHAIN.
DOMAIN 309 436
RICIN B-TYPE LECTIN 1.
DOMAIN 439 563
RICIN B-TYPE LECTIN 2.
REPEAT 319 361
1-ALPHA.
REPEAT 362 402
1-BETA.
REPEAT 405 437
1-GAMMA.
REPEAT 450 485
2-ALPHA.
REPEAT 489 528
2-BETA.
REPEAT 531 558
BY SIMILARITY.
ACT_SITE 200 200
DISULFID 282 306
INTERCHAIN (BY SIMILARITY).

FT	DISULFID	322	341	BY SIMILARITY.
FT	DISULFID	365	382	BY SIMILARITY.
FT	DISULFID	453	466	BY SIMILARITY.
FT	DISULFID	492	509	BY SIMILARITY.
FT	CARBOHYD	34	34	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	259	259	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	437	437	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	331	331	F -> T (IN REF. 2).
FT	CONFLICT	362	362	N -> D (IN REF. 2).
FT	CONFLICT	374	374	R -> G (IN REF. 2).
FT	CONFLICT	404	404	R -> T (IN REF. 2).
FT	CONFLICT	552	552	F -> V (IN REF. 2).
SQ	SEQUENCE	564 AA:	62851 MW:	D455F2A72F609759 CRC64:

Query Match 16.8%; Score 271.5; DB 1; Length 564;
Best Local Similarity 28.7%; Pred. No. 4e-14;
Matches 77; Conservative 47; Mismatches 107; Indels 37; Gaps 7;
QY 28 ITFDAGNATINKYATFMSURNOAKDKPKLCYGIPIMLPDTNSTP---KYLLVKILOGANIK 84
DB 33 INETIADATVESVTNFTRAVRSILTTGADVRRHEIPVLPNRVGLPISQRFILVELLSNIAEL 92
QY 85 TITLMLRRNNLYVNG-----YSDPENGKCRHYHFNIDITSTERTTOVENTLSSSS 134
DB 93 SVTLALDYTNAYVYVCCRAGNSAYFFHPDNOEDAEALPHLP-----TDQVN----- 137
QY 135 SRVAMSYNNSLYPTMEKKAENSRNOVQIGIQLSSDGIKI--SGVDSFPVKTEAPFLI 192
DB 138 ---SETAFGNGYDRLEQJGL--RENIEIGTGTPLEDAISALYYSTCGTQIPIHARSFM 192
QY 193 VAIQMSVSEARFKYIENOVKT--NFNRAFYPPDPKVINLEEKWKGIKSEIHNNAKNGALPKP 250
DB 193 VCIONISEAAHQVIEGEMTRIRYNRRSAPDPSVITLNSWGRSLTAIOESNOGAFASP 252
QY 251 LELVDAGTKWIKLVKDEINRDVALIAY 278
DB 253 IQLORNGSKFNVDVDSILIPITIALMY 280

Search completed: May 28, 2003, 09:56:38
Job time : 27 secs

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EMBL: X59256; CAA41949.1; --
PIR: S17932; S17932.
HSP: P10297; 10CG.
InterPro: IPR001574; RIP.
Plam: PF00161; RIP; 1.
PROSITE: PS00275; SHIGA_RICIN; 1.
Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
Multigene family.
NON_IPR 1
ACT_SITE 148 148 BY SIMILARITY.
SEQUENCE 236 AA; 26591 MW; DE3D68BA50FCE054 CRC64;
Query Match 17.6%; Score 285; DB 1; Length 236;
Best Local Similarity 35.9%; Pred. No. 1.le-15;
Matches 89; Conservative 41; Mismatches 88; Indels 30; Gaps 11;

53 OPKLCVCIGIP-LPDTNSTKYLKLVKLOGANLKTITMLRNNLYVMGYSDPFNCNKC- 110
111 YHFNIDITSTERTDVENTLCSRSSRVAMSYNSLYPTMEKAEV---NSRQVOVLGI 166
60 YFGTEITSALT---TLPEATVANOKALEYTEDVOSIEKNAKITTEGDKTRKELGLGI 115
167 QILSS---DIGKISGVDSFPVKTEAFELVAIQMVSAARFYIENQVKTNFNRAFYDPD 223
116 NLLSTLDVANKRV---VKNEARELLIAQMTAEAREFYIONLVTKNFKENSED 171
224 KVINLEEKWKISEAIIH-NAKNGALPPELVDAKGTWIVLRVDEINROVALKYNGT 282
172 KVIQFVNSKISAKIYGDANKGVFNKDYDFGFEK-----VRQVKDL--QNGLLMYLG-- 222
-283 COTTYONA 290
223 --TTPNNA 228

RESULT 14
IPP MIRJA STANDARD; PRT; 278 AA.
C P21326;
T 01-MAY-1991 (Rel. 18, Created)
T 01-DEC-1992 (Rel. 24, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
E Antiviral protein MAP precursor (Ribosome-inactivating protein) (cRNA
S N-glycosidase) (EC 3.2.2.22).
S Mirabilis jalapa (Garden four-o'clock).
S Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
S Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
S Caryophyllidae; Caryophyllales; Nyctaginaceae; Mirabilis.
NCBI_TaxID=3538;
[1]
[2]
SEQUENCE FROM N.A.
MEDLINE-93197126; PubMed=2022657;
Kataoka J., Habuka N., Furuno M., Miyano M., Takanami Y., Koizumi A.;
"A genomic gene for MAP, a ribosome-inactivating protein from
Mirabilis jalapa, contains an intron.";
J. Biol. Chem. 266:8426-8430(1991).
[2]
SEQUENCE FROM N.A.
MEDLINE-93197126; PubMed=8451171;
Kataoka J., Miyano M., Habuka N., Masuta C., Koizumi A.;
"A genomic gene for MAP, a ribosome-inactivating protein from
Mirabilis jalapa, contains an intron.";
Nucleic Acids Res. 21:1035-1035(1993).

[3]
SEQUENCE OF 29-278.
MEDLINE-89214063; PubMed=2708328;
Habuka N., Murakami Y., Noma M., Kudo T., Horikoshi K.;
"Amino acid sequence of Mirabilis antiviral protein, total synthesis
of its gene and expression in Escherichia coli.";
J. Biol. Chem. 264:6629-6637(1989).
CC -!- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
CC SYNTHESIS IN VITRO.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).

EMBL: D10227; BAA01079.1;
EMBL: D10569; BAA01425.1;
PIR: A39817; A39817.
PIR: S36928; S36928.
HSP: O03464; IAPA.
InterPro: IPR001574; RIP.
Plam: PF00161; RIP; 1.
PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 28
FT CHAIN 29 278 ANTIVIRAL PROTEIN MAP.
FT ACT_SITE 196 196 BY SIMILARITY.
FT DISULFID 64 248 POTENTIAL.
FT CONFLICT 35 35 1 -> L (IN REF. 1).
FT CONFLICT 58 58 A -> V (IN REF. 1).
FT CONFLICT 180 180 V -> C (IN REF. 1).
FT CONFLICT 218 218 D -> G (IN REF. 1).
SQ SEQUENCE 278 AA; 31132 MW; BDB9E08E5D2F92D CRC64;

Query Match 17.3%; Score 279.5; DB 1; Length 278;
Best Local Similarity 32.5%; Pred. No. 3.7e-15;
Matches 92; Conservative 44; Mismatches 128; Indels 19; Gaps 11;
QY 2 KVMVLVVVLLIAM-LIAAPTSTCA--INTI-TFDAGNATINKYATPMSLRNOAKDKPKL 57
DB 6 KVFPELLTITWITWYAVNPQSKAAPTLETIASLDLNNPT--TYLSFITNIRTKVADKTEQ 63
QY 58 CYGIPMLPDPNSTKYLLVAVKLOGANLKTITMLRNNLYVMGYSDPFNCNKCRIYIFNDI 117
DB 64 C-TTQKISKI-FTQYSYDILVSVSTOKITLADMAVLVYLVGYSDIAN-NKGRAFFPKDV 120
QY 118 TSTERTDVENTLCSRSSRVAMSYNSLYPTMEKAEVMSRNOVQLGTQTLSSDICKIS 177
DB 121 TEA---VANFFPGATGTTNKIKLTFGSGULEKNGGLRKDN--PLGIFLENSIVNVI 174
QY 178 GVDSFPVKTEAFELVAIQMVSAARFYIENQVKTNFNRAFYDPDKVIVNLEEKWKINE 237
DB 175 G-KAGDVKKQAKFELLAIQMVSAARFYISDKIPSEKYEEVTVDEYMTALENNWAKIST 233
QY 238 AIHNAK---NCALPKPELVIAKCTKWIVLRVDEINROVALIK 277
DB 234 AVYNSKPESTTTATKCOLATSPVITSPWIEKTVGEIKLVMLGLK 276

RESULT 15
AGGL_RICCO
ID AGGL_RICCO STANDARD; PRT; 564 AA.
AC P06750;
DT 01-JAN-1988 (Rel. 06, Created)

67 LTTGADVREHPVLPNVRGLPINORFILVELSNHAEISVTLALDVTNAYVYCYR---AGN 123
108 KCRY-----HIFNDITSTERTDVENTLCSSSSSRVAMSYNLSLYPTMEKA 154
124 SAYFFHPDNQDEAEATHLF-----TDVN-----RYTAFGCGN--YDRLEOLA 165
155 EVNSRNOVOLGIQILSSDIGI-----SGVDSFPVKTEAFFLLVAIQMSEARFKYIENQ 210
166 G-NLRENIEELGNGLEEAISALYYSTGTQTLTARSF--IICIMISEARFPYIEGE 222
211 VKT--NENRATYPPKVINLEEKKIKSEIHNKNGALPKPLELVDAKQKIWIYLRVDE 268
223 WRTIRYMRGAPDSVITLNSWGRSLTQESNQAFASPIQLORRNGSKFSYDVYSI 282
269 INROVALKY 278
283 LIPITIALMVY 292

RESULT 12

RIP1_TRIAN STANDARD: PRT: 294 AA.
P56626; Q93Q77;
15-DEC-2000 (Rel. 37, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Type I ribosome-inactivating protein trichoanguina precursor (rRNA N-glycosidase) (EC 3.2.2.22) (RIP) (Trichoanguin).
TCA.
Trichosanthes anguina (Snake gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI_TaxID=50544;
[1]
SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
STRAIN=cv. Anguina; TISSUE=Seed;
MEDLINE=99132006; PubMed=993118;
Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H., Lin J.-Y.;
"Purification, characterization and molecular cloning of trichoanguin, a novel type I ribosome-inactivating protein from the seeds of Trichosanthes anguina.";
Biochem. J. 338:211-219(1999).
[2]
SEQUENCE OF 20-264.
TISSUE=Seed;
Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;
"Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from Trichosanthes anguina seeds.";
J. Biomed. Sci. 3:178-186(1996).
-!- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RRNA IN RIBOSOMES.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.

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EMBL: AF055086; AAD02686.1;
HSSP: P33185; LBRY.
InterPro: IPR001574; RIP.
Pfam: PF00161; RIP; 1.
PRINTS: P000396; SHIGARICIN.
PROSITE: P500275; SHIGA-RICIN; FALSE_NEG.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;

KW Glycoprotein: Signal_19
FT SIGNAL 1 264
FT CHAIN 1 264
FT TYPE I RIBOSOME-INACTIVATING PROTEIN
FT TRICHOANGUINA.
FT PROPEP 265 294
FT ACT_SITE 177 177
FT ACT_SITE 180 180
FT CARBOHYD 70 70
FT CARBOHYD 220 220
FT CONFLICT 51 51
FT CONFLICT 65 65
FT CONFLICT 84 84
FT CONFLICT 152 152
FT CONFLICT 174 174
FT CONFLICT 245 245
SQ SEQUENCE 294 AA: 32234 MW: 24488B7CE3290994 CRC64;
BY SIMILARITY.
N-LINKED (GLCNAC...) (PROBABLE).
N-LINKED (GLCNAC...) (PROBABLE).
C -> Y (IN REF. 2).
W -> R (IN REF. 2).
N -> D (IN REF. 2).
A -> S (IN REF. 2).
C -> S (IN REF. 2).
N -> H (IN REF. 2).

Query Match 18.6%; Score 300; DB 1; Length 294;

Best Local Similarity 30.0%; Pred. No. 9.3e-17;

Matches 85; Conservative 57; Mismatches 113; Indels 28; Gaps 10;

QY 12 IAMLIAAPTSTCAINTITFDAGNATINKYATFMESLRNQAKDPKLCYGIPLPDTNSTP 71
DB 8 LAISLGSPT---AIGDSFSLSTATKKSYSSEITQLRDALPTQCTVC-GIPLLPSTANGS 63
QY 72 KYL-LVKLOGANLKITILMLRRNNLYVMGY-SDPENGKCRVHIFNDITSTERTDVNTIL 129
DB 64 QMRFENITNTDETIVAVNTVIVAYRADAVS-----YFED---TPAENAKLIF 134
QY 130 CSSSSSRVAMSYNLSLYPTMEKKAENSRNQVQIGIQLSSDIGKISGVNSFPVKTKAF 189
DB 115 ACTKTKVLPYSUNYDKLQSVGKQ-----RDMIELGIPALSS---AITNMVYDYVSIAA 166
QY 190 FILVALQMVSAAREFYIENQVKNFNENAFYDPDKVINLEEKWKGLSEAIHNK---NCA 246
DB 167 ALLVLIOCTAAARYKIIEQVSSH[SSNFYPNQAVISLENKKGALSQKIQIQTANRTGIGQ 226
QY 247 LPKPLEFLVDAGTKWIVLVRVDG--INROVALKYVNGTCOTTY 287
DB 227 FENPVELYNDQTRFSTNTSAGVVGKGNIKLULLYYKASVGSEY 269

RESULT 13

RIP3_SAPOF
ID RIP3_SAPOF STANDARD: PRT: 236 AA.
AC P27560;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-3 (SAP-3) (SO-3) (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
GN SAP3.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=92049247; PubMed=1719367;
RX Fordham-Skellon A.P., Taylor P.E., Hartley M.R., Croy R.K.D.;
RT "Characterisation of saporin genes: in vitro expression and ribosome inactivation".
RL Mol. Gen. Genet. 229:460-466(1991).
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR PHARMACOLOGICAL APPLICATIONS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.

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[illegible]

Best Local Similarity 28.7%; Pred. No. 8.3e-17;
Matches 89; Conservative 48; Mismatches 108;
Indels 65; Cons 11;

10	TLIAWLIAMPTSTCAINT-----ITFDAGNATINKVATEMESLKNO	50
	: : : : : :	:
7	TIVLWMVAVALUGUSTSCWSFTLEDNNIFIE-PLINFTTAGATVOUSYTNFIRAVKGR	66
	: : : : : :	:
51	AKDPKLCKCYGIDHPIPFNTSP---KYLLVKLGICANIKJLTJLMLRRNNILVMGYSDHPEN-N	107
	: : : : : :	:

RT RT FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
RL J. Biol. Chem. 268:6541-6548 (1993).
CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.

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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X69131; CAA48885.1;
CC EMBL: X69132; CAA48886.1;
CC HSSP: P10297; IQCG.
CC InterPro: IPR001574; RIP.
CC Pfam: PF00161; RIP; 1.
CC PROSITE: PS00275; SHIGA_RICIN; 1.
CC Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
CC Multigene family.
CC ACT_SITE 176 176 BY SIMILARITY.
CC SEQUENCE 253 AA: 28556 MW: 538693E13D0F594D CRC64:

Query Match 20.8% Score 337; DB 1; Length 253;
Best Local Similarity 35.5% Pred. No. 8.8e-20;
Matches 93; Conservative 50; Mismatches 99; Indels 20; Gaps 9;

25 INTITDAGNATINKYATPMESLRNOAKPKLKCVCIPM-LPDNTSTPKYLKLOGANL 83
1 VTSITLDLVNTPAGOVSPVDKIRNNKPNLKYGGTDIAVIGPPSKKFLRINFOSR- 59
84 KTTILMLRNNLYVMGYSDPFNGNKR-YHIFNDITSTERTDVENTLSCSSSRVAMSN 142
60 GTVSLGCKNDLVVAYLAMDNNTNVRAYFRSEITSAELT-----ALFPEATANOKALE 115
143 YNSLYPTMEKKAEEV-----NSRNQVQLGQILSSDICKISGVDSFPVKTEAFELLVAIQW 198
116 YTEDYOSIEKNAQITGGDKSRKELGIGDILLTSMEAVN-KKRVVKNARELLIAQMT 174
199 SEAAEFKYTENOVKNFNRAPYDPKVINLEEKWGISPAIH-NAKNGALPKPLGLVDK 257
175 AEVAPFRYTONLVNFPNPKNSKNVIOFEVSWRKISTAIYGDANKGVFNKDYDFGCK 234
258 GTKWIVLRVDEINROVALLKYV 279
235 -----VRQVKDL--QNGLLMYL 249

RESULT 9
ID RIP7 SAPOF STANDARD: PRT: 253 AA.
041391
6-OCT-2001 (Rel. 40. Created)
6-OCT-2001 (Rel. 40, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN SAPORIN-7 (SO-7) (SAP-7) (rRNA N-
glycosidase) (EC 3.2.2.22).
SAP7.
Saponaria officinalis (Common soapwort).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllaceae; Caryophyllaceae; Saponaria.
NCBI_TaxID=3572;
SEQUENCE FROM N.A.
TISSUE: Leaf;
MEDLINE=93203250; PubMed=8454624;
Barthelemy I., Martineau D., Ong M., Matsunami R., Ling N.,
Benatti L., Cavallaro U., Soris M., Lappi D.A.;
The expression of saporin, a ribosome-inactivating protein from the

RT RT plant Saponaria officinalis, in Escherichia coli.;
RL J. Biol. Chem. 268:6541-6548 (1993).
CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.

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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

CC EMBL: X69131; CAA48885.1;
CC EMBL: X69132; CAA48886.1;
CC HSSP: P10297; IQCG.
CC InterPro: IPR001574; RIP.
CC Pfam: PF00161; RIP; 1.
CC PROSITE: PS00275; SHIGA_RICIN; 1.
CC Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
CC Multigene family.
CC ACT_SITE 176 176 BY SIMILARITY.
CC SEQUENCE 253 AA: 28553 MW: 161319102AB20539 CRC64:

Query Match 20.8% Score 336; DB 1; Length 253;
Best Local Similarity 35.5% Pred. No. 1.1e-19;
Matches 93; Conservative 51; Mismatches 98; Indels 20; Gaps 9;

25 INTITDAGNATINKYATPMESLRNOAKPKLKCVCIPM-LPDNTSTPKYLKLOGANL 83
1 VTSITLDLVNTPAGOVSPVDKIRNNKPNLKYGGTDIAVIGPPSKKFLRINFOSR- 59
84 KTTILMLRNNLYVMGYSDPFNGNKR-YHIFNDITSTERTDVENTLSCSSSRVAMSN 142
60 GTVSLGCKNDLVVAYLAMDNNTNVRAYFRSEITSAELT-----ALFPEATANOKALE 115
143 YNSLYPTMEKKAEEV-----NSRNQVQLGQILSSDICKISGVDSFPVKTEAFELLVAIQW 198
116 YTEDYOSIEKNAQITGGDKSRKELGIGDILLTSMEAVN-KKRVVKNARELLIAQMT 174
199 SEAAEFKYTENOVKNFNRAPYDPKVINLEEKWGISPAIH-NAKNGALPKPLGLVDK 257
175 AEVAPFRYTONLVNFPNPKNSKNVIOFEVSWRKISTAIYGDANKGVFNKDYDFGCK 234
258 GTKWIVLRVDEINROVALLKYV 279
235 -----VRQVKDL--QNGLLMYL 249

RESULT 10
ID RIP7 SAPOF STANDARD: PRT: 316 AA.
041391
6-OCT-2001 (Rel. 40. Created)
6-OCT-2001 (Rel. 40, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN SAPORIN-7 (SO-7) (SAP-7) (rRNA N-
glycosidase) (EC 3.2.2.22).
SAP7.
Gelonium multiflorum (Euphorbiaceae himalayana).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eucosids; Malpighiales; Euphorbiaceae; Gelonium.
NCBI_TaxID=39795;
SEQUENCE FROM N.A.
MEDLINE=94085781; PubMed=7916721;
Nolan P.A., Garrison D.A., Reiter M.;
Cloning and expression of a gene encoding gelonin, a ribosome-
inactivating protein from Gelonium multiflorum.

09978274
 Multigene family. 24
 SIGNAL 1 25
 CHAIN 25 292
 ACT_SITE 200 200
 VARIANT 72 72
 SEQUENCE 292 AA: 32810 MM: FAL43C0E1BE88976 CRC64:

Query Match 23.0%: Score 372; DB 1; Length 292;
 Best Local Similarity 35.4%: Pred. No. 1.8e-22;
 Matches 108; Conservative 52; Mismatches 107; Indels 38; Gaps 12:

4 MLVVVVTLIAWLI---AAPTSTCAINTITDAGNATINKYATFESLRNOAKDKPKLCYGG 60
 1 MKIYVATIAWILLOFSAWTTDAVTSITLDLVNPTAGQYSSFYDKIRNNVKDPNLKXGG 60
 61 IPM-LPDTNSTPKYLLVKLGQANIKTITMLRRNNLYVMGYSDPENGKCR-YHFNDDI 118
 61 TDIAVIGPPSKDKELRINFQSSR-GTVSLGLKRONLYVAVLAYLAMDNTNVRAYFKSEIT 119
 119 STERTDVENTLCSSSSSRVAMSYNSLYPTMEKAEV-----NSRNOVOLGIGL---SS 171
 120 SAELT-----ALFPETATANKALEYTDYOSIERNAQITQDQSRKELGLGIDLLLTME 175
 172 DIGKISGVDPFPVTEAFFLLVAIOMVSEARFYIENQVKTNFNRAFYDPKVINLEEK 231
 176 AVNKKARV---VKNREAFLLIAOMTAEVARFYIQLNLTNFKNFKDSNKNVQIFEV 231
 232 WCKTSEAIH-NAKNGALPKPLELVDAKGTWKIVLRVDEINRDVALLKIV-----NG 281
 232 WRKISTAIYGDANKGVFNKDYDFGK-----VRQVKDL--QMGLLMLYGLRKPSSNEANS 284
 282 TCQTT 286
 285 TAYAT 289

DIACA STANDARD: PRT: 293 AA.
 P24476:
 01-MAR-1992 (Rel. 21, Created)
 01-DEC-1992 (Rel. 24, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 Antiviral protein DAP-30 precursor (Ribosome-inactivating protein)
 (RNA N-glycosidase) (EC 3.2.2.22) (Dianthin 30)
 Dianthus caryophyllus (Carnation) (Clove pink)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
 NCBI_TaxID=3570;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=91355219; PubMed=1840496;
 Legname G., Bellio P., Gromo G., Modena D., Keen J.N., Roberts L.M.,
 Lord J.M.:
 "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome
 inactivating protein from Dianthus caryophyllus.";
 Biochim. Biophys. Acta 1090:119-122(1991).
 [2]
 SEQUENCE OF 24-82.
 TISSUE=Leaf;
 MEDLINE=92037998; PubMed=1936243;
 Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P.,
 Huang H.-I., Chen H.-C.:
 "A new class of anti-HIV agents: CAP31, DAPS 30 and 32.";
 FEBS Lett. 291:139-144(1991).
 HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
 AND TO INTACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INFECTION AND
 REPLICATION.
 CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUDEFAMILY.
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL: X59260; CAA41953.1; ALT_SEQ.
 DR PIR: S17519; S17519.
 DR HSSP: 003464; IAPA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RTP.1.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_HICIN.1.
 DR Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase;
 KW Toxin; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 293 ANTIVIRAL PROTEIN DAP-30.
 FT ACT_SITE 200 200 BY SIMILARITY.
 SQ SEQUENCE 293 AA: 32717 MM: AC85AAAC8725D4F2 CRC64:

Query Match 21.4%: Score 345.5; DB 1; Length 293;
 Best Local Similarity 34.5%: Pred. No. 2.3e-20;
 Matches 100; Conservative 52; Mismatches 108; Indels 29; Gaps 12:

QY 4 MLVVVVTLIAWLIAPTS--TCAINTITDIAGNATINKYATFESLRNOAKDKPKLCYGG- 60
 DB 1 MKIYVATIAWILLOFSAWTTDAATAYTLNLNAPSASQYSSFLDQIRNVRDTS- 171
 QY 61 --IPMLPDTNSTPKYLLVKLGQANIKTITMLRRNNLYVMGYSDPENGKCR-YHFNDDI 117
 DB 60 TDVAVIGAPSTTDKELNFOGPK-GTVSLGIRRENTYVAVLAYLAMDANVNRKATYFKNQ 118
 QY 118 TSTERTDVENTLCSSSSSRVAMSYNSLYPTMEKAEV-----NSRNOVOLGIGLSSDI 173
 DB 119 TSAELTALFPEVVANQKQ----LEYGEDYQAIENAKITTDQSRKELGLGIGLNL--- 171
 QY 174 KISGVIS--FPVTEAFFLLVAIOMVSEARFYIENQVKTNFNRAFYDPKVINLEEK 231
 DB 172 TMDGVNKKVVRVDEARFLLIATQTAARFYIQLNLTNFKNFKDSNKNVQIFEV 231
 QY 232 WCKTSEATH-NAKNGALPKPLELVDAKGTWKIVLRVDEINRDVALLKIV 279
 DB 232 WSKISTALFGDCKNGVFNKDYDFGK-----VRQAKDL--QMGLLKL 273

RESULT 8
 RIP5_SAPOF STANDARD: PRT: 253 AA.
 AC Q41389:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein saporin-5 (PC 3.2.2.22) (SAP-5) (rRNA N-
 DE glycosidase).
 GN SAP5.
 OS Saponaria officinalis (Common soapwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
 OC NCBI_TaxID=3572;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Leaf;
 RX MEDLINE=91303250; PubMed=8454624;
 RA Barthelemy T., Martineau D., Ong M., Matsuami K., Ling N.,
 Benatti L., Cavallaro U., Sorla M., Lippi D.A.:
 "The expression of saporin, a ribosome-inactivating protein from the
 plant Saponaria officinalis, in Escherichia coli.";
 J. Biol. Chem. 268:6541-6548(1993).

Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

25 INTITFDAGNATINATYATFMSLRNOAKDPKLCYCIPLMPTDNTSPKYLVLKQGANLK 84
 1 INTITFDAGNATINATYATFMSLRNEAKOPSLKCYGIPMLPTNSTIKYLLVKLOASLK 60

85 TITLRRNNLVVMGVSDPFGNCKRYHIFNDITSTERTDVENTLCSSSSRVAMSINYN 144
 61 TITLRRNNLVVMGVSDPYD-NKRYHIFNDIKGTEYSDVENTLCPSSNPRVAKPDINTN 119

145 SLYPTMEKAEYNSRNOVLGQIOILSSDICKISGVDSFFVKTEAFELLVAIQWVSAARE 204
 120 GLYPTLEKKAGVTSRNEVLGQIQLSSDICKISGVDSFFTEKIEAKELLVAIQWVSAARE 179

205 KYENOVKTNFRNRYPDPKVNLNEEKWKISIAIHNAKNGALPKPELVDKAGTKWIVL 264
 180 KYENOVKTNFRNRYPDPKVNLNEEKWKISIAIHNAKNGALPKPELKNADGTKWIVL 239

265 RVDEINROVALLKYNVGTCTT 286
 240 RVDEIKPDVGLLNVNGTCTT 261

RESULT 4

RIP2_PHYAM STANDARD; PRT: 310 AA.

16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 Antiviral protein 2 precursor (PAP-II) (Ribosome-inactivating protein) (rRNA N-glycosidase) (EC 3.2.2.22).
 PAP2 OR PAP1.
 Phytolacca americana (Common pokeweed) (Virginian pokeweed).
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
 NCBI_TaxID=3527;
 (1)
 SEQUENCE FROM N.A.
 TISSUE=Leaf;
 MEDLINE=94307398; PubMed=6091760;
 Poyet J.-L., Radom J., Hoeveler A.;
 "Isolation and characterization of a cDNA clone encoding the pokeweed
 antiviral protein II from Phytolacca americana and its expression in
 E. coli";
 FEBS Lett. 347:268-272(1994).
 (2)
 SEQUENCE OF 26-55.
 TISSUE=Leaf;
 MEDLINE=85023392; PubMed=6091760;
 Bjorn M.J., Larrick J., Piatok M., Wilson K.J.;
 "Characterization of translational inhibitors from Phytolacca
 americana. Amino-terminal sequence determination and antibody-
 inhibitor conjugates";
 Biochim. Biophys. Acta 790:154-163(1984).
 !- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. INHIBITS PROTEIN
 SYNTHESIS IN BOTH PROKARYOTES AND EUKARYOTES.
 !- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 !- TISSUE SPECIFICITY: EXPRESSED IN LATE SUMMER LEAVES.
 !- DEVELOPMENTAL STAGE: EXPRESSED PROGRESSIVELY WITH THE AGING OF THE
 PLANT.
 !- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 TYPE 1 RIP SUBFAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL: X78628; CA55342.1;
 DR HSSP: Q03464; IAPA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP: 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00375; SHIGARICIN.
 KW Plant defense: Antiviral; Protein synthesis inhibitor; hydrolase;
 KW Toxin; Signal.
 FT SIGNAL. 1 25
 FT CHAIN. 26 ?
 FT PROPEP 310
 FT ACT_SITE 157 197
 FT DISULFID 57 284
 FT DISULFID 106 123
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 SQ SEQUENCE 310 AA: 34694 MW: 40380010725909F CRC64;

Query Match 31.6%; Score 511; DB 1; Length 310;

Best Local Similarity 39.9%; Pred. No. 1.7e-33;
 Matches 130; Conservative 53; Mismatches 111; Indels 32; Gaps 14;

QY 1 MKVMLVVVVTGLIAWLIAPTSTCAINTITFDAGNATINATYATFMSLRNOAKDPKLCYVG 60
 DB 3 MKVLEVVGLAISIMLMITPP---ASSNIVDFDENATPETYSNFLTSLREAVKDKKLTLNG 59

QY 61 IPLMPTNSTPKYLVKLGANLKTITLMLRRNNLVVMGVSDPFGNCKRYHIFNDITST 120
 DB 60 MINATTLTEQPKYVILVDLKFSG-TFTLAIRGNLYIEGYSDIYNG-KCRYHIFND---- 113

QY 121 EMTDVENTLCSSSSR--VAMSYNSLYPTMEKAEYNSRNOVLGQIOILSSDICKING 178
 DB 114 SESDAQETVCPGDKSKPGTQNNIPYEKSYKMGESKG--GARTKLGKGLTKLSRWCKING 171

QY 179 VDSFP---VKTEAFELLVAIQWVSAAREFYENOVKTNFRA--FYDDPKVNIHEMW 232
 DB 172 KQATDOKQYKNEAEFLLIAVOMVTVEASREKYIENKAKAFODANGYQDPKALISLEKNW 231

QY 233 GKISEAHNAKNG----ALPKPELVDKAGTKWIVLRVDEINROV-ALLKYNVGTCTT 286
 DB 232 DSVSKVL--AKVGTSDUSTVITLPCDLKDKNKPKWTATMNLKNOIMALLTHV--TCNV- 286

QY 287 YONAFMSOVIISTYNYMSNLGLDFE 312
 DB 287 -XSSMPETMSYVYNTSISNLGE-FE 310

RESULT 5

RIP6_SAPOF STANDARD; PRT: 299 AA.

AC P20656; Q41392;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein saporin-6 precursor (SAP-6) (SU-6)
 DE (rRNA N-glycosidase) (EC 3.2.2.22).
 GN SAP6.
 OS Saponaria officinalis (Common soapwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
 OX NCBI_TaxID=3572;
 RN (1)
 RP SEQUENCE OF 1-283 FROM N.A., AND SEQUENCE OF 25-115; 206-213 AND
 RP 234-277.
 RC TISSUE=Leaf;
 RX MEDLINE=89338421; PubMed=2547612;
 RA Benatti L., Saccardo M.R., Dani M., Nitti G., Sassano M.,
 RA Lorenzetti R., Lappi D.A., Sorla M.;
 RT "Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-
 RT inactivating protein from Saponaria officinalis";
 RL Eur. J. Biochem. 183:463-470(1989).
 RN (2)
 RP SEQUENCE OF 25-277 FROM N.A.

Miyano M.:
 "X-ray structure of a pokeweed antiviral protein, coded by a new genomic clone, at 0.23-nm resolution. A model structure provides a suitable electrostatic field for substrate binding."
 Eur. J. Biochem. 225:369-374(1994).

FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN SYNTHESIS IN VITRO. HAS ALSO BEEN SHOWN TO INHIBIT THE REPLICATION OF MAMMALIAN VIRUSES. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR SUICIDE UPON INVASION BY A VIRUS.

!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

!- SUBUNIT: MONOMER.

!- SUBCELLULAR LOCATION: Cell wall.

!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.

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EMBL: D10600; BAA01451.1;

PIR: S28421; S28421

POB: IAPA; 31-JAN-94.

InterPro: IPR001574; RIP.

Pfam: PF00161; RIP; 1.

PROSITE: PS00275; SHIGA_RICIN; 1.

Plant defense: Antiviral; protein synthesis inhibitor; hydrolase.
 Toxin; Signal; Cell wall; 3D-structure.

SIGNAL 1 24 BY SIMILARITY.

CHAIN 25 285 ANTIVIRAL PROTEIN ALPHA.

PROPEP 286 294

ACT_SITE 199 199

DISULFID 58 282

DISULFID 108 130

STRAND 28 31

STRAND 32 34

HELIX 37 51

STRAND 57 58

TURN 59 60

STRAND 61 63

TURN 67 68

TURN 73 79

TURN 81 82

STRAND 85 91

TURN 92 94

STRAND 97 104

TURN 105 106

STRAND 107 113

TURN 114 115

TURN 119 129

STRAND 136 138

STRAND 141 141

HELIX 147 154

TURN 155 155

TURN 158 160

STRAND 163 163

TURN 165 175

TURN 176 177

HELIX 183 195

TURN 196 197

TURN 198 202

TURN 204 212

TURN 213 215

TURN 218 218

STRAND 222 240

STRAND 242 242

TURN 243 244

TURN 245 253

TURN 255 255

FT STRAND 259 264
 FT HELIX 265 271
 FT STRAND 275 275
 SQ SEQUENCE 294 AA: 33069 MW: F2EC27724FA85596 CRC64:
 Query Match 68.9% Score 1113.5; DB 1: Length 294;
 Best Local Similarity 75.4% Pred. No. 2.2e-81;
 Matches 221: Conservative 27; Mismatches 42; Indels 3; Gaps 3;
 Oy 1 MKVMIVVVVTVLWMLIAAPTSTCAINTITFDAGNATINKYATPESLNQAKDPKIKYGV 60
 Db 1 MKVMIVVVVTVLWMLIAAPTSTCAINTITFDAGNATINKYATPESLNQAKDPKIKYGV 60
 Oy 61 IPMLPDTNSTPKYLLVKKLGANIKTITLMLRNNNLYVNGYSDPENGKCRVHFNDET-S 119
 Db 61 IPMLPNTNLTPKYLLVLTQDSSKTTITLMLRNNNLYVNGYADTYNG-KCRVHFNDET-SNT 119
 Oy 120 TERTDVENTLSSSSSRVAMSTINYSLYPTMEKKAENSRNOVQLGILLSSDICKISCV 179
 Db 120 TERNDDVMTTLCVNPSSRVGKNNYVSSYPALEKKVG-HPRSQVQLGILLNSGICKLYGV 178
 Oy 180 DSFPVKTEAFFLLVAIONVSEARPKYIFENOVKTNFNAFYDPDKVINLEEKWCKISEAI 239
 Db 179 DSFTKTEAFELLLVAIONVSEARPKYIFENOVKTNFNAFYDPDKVINLEEKWCKISEAI 238
 Oy 240 HNAKNCALPKPLEIWDKGTWIVLKVDEINRDVALKYVNGTCOTTYQAMF 292
 Db 239 INAKNGALTSPLKKNANGSKWIVLVRVDDIEPDVGLLYVNGTCOTTYQAMF 291

RESULT 3

RIPS_PHYAM STANDARD: PRT: 261 AA.
 AC P23339:
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Antiviral protein S (PAP-S) (Ribosome-inactivating protein) (rRNA
 DE N-glycosidase) (EC 3.2.2.22).
 OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
 OC Caryophyllales: Caryophyllaceae: Phytolaccaceae: Phytolacca.
 OX NCBI_TaxID=3527;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Seed;
 RX MEDLINE=91242096; PubMed=1368643;
 RA Kung S.S., Kimura M., Funatsu G.:
 RT "The complete amino acid sequence of antiviral protein from the seeds
 of pokeweed (Phytolacca americana)."
 RL Agric. Biol. Chem. 54:3301-3318(1990).
 CC !- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
 SYNTHESIS IN VITRO.
 CC !- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC !- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC PIR: J00401; J00401.
 DR HSP: Q03464; IAPA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGA_RICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; hydrolase;
 Toxin.

FT ACT_SITE 175 175 BY SIMILARITY.
 FT DISULFID 34 258
 FT DISULFID 84 105
 SQ SEQUENCE 261 AA: 29200 MW: D88B9962FE8399D CRC64:

Query Match 67.8% Score 1096.5; DB 1: Length 261;
 Best Local Similarity 82.8% Pred. No. 4.3e-80.

[6] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=94016586; PubMed=8411176;
Monzinger A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D.:
"The 2.5 A structure of pokeweed antiviral protein.";
J. Mol. Biol. 233:705-715(1993).
[7] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-284.
MEDLINE=94213120; PubMed=10493577;
Kurinov I.V., Myers D.E., Irvin J.D., Uckun F.M.:
"X-ray crystallographic analysis of the structural basis for the
interactions of pokeweed antiviral protein with its active site
inhibitor and ribosomal RNA substrate analogs.";
Protein Sci. 8:1765-1772(1999).
-!- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
SYNTHESIS IN VITRO.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- TISSUE SPECIFICITY: SPRING LEAVES AND ROOTS.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.

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or send an email to license@isb-sib.ch).

EMBL: X55383; CAA39054.1;
PIR: S02792; S02792;
PIR: S13469; S13469;
PDB: 1PAF; 31-JAN-94.
PDB: 1PAG; 31-JAN-94.
PDB: 1QCI; 15-SEP-99.
PDB: 1QCG; 15-SEP-99.
PDB: 1OCJ; 15-SEP-99.
InterPro: IPR001574; RIP.
Pfam: PF00161; RIP; 1.
PRINTS: PR00396; SHIGARICIN.
PROSITE: PS00275; SHIGA_RICIN; 1.
Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase;
Toxin; Signal; 3D-structure.
SIGNAL 1 22
CHAIN 23 285
PROPEP 286 313
ACT_SITE 198 198
DISULFID 56 281
DISULFID 107 128
STRAND 25 29
HELIX 35 49
STRAND 55 56
TURN 57 58
STRAND 59 61
TURN 65 66
STRAND 71 78
HELIX 79 81
STRAND 82 89
TURN 90 93
STRAND 94 102
TURN 103 105
STRAND 106 112
TURN 113 114
TURN 117 117
HELIX 118 127
TURN 131 132
STRAND 134 136
STRAND 139 139
HELIX 145 152
TURN 153 153
TURN 157 158
STRAND 162 162

ANTIVIRAL PROTEIN I.

BY SIMILARITY.

RESULT 2

RIPA_PHYAM

ID	RIPA_PHYAM	STANDARD:	PRT:	294 AA.
AC	Q03464;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Antiviral protein alpha precursor (PAP-alpha) (Ribosome-inactivating protein) (rRNA N-glycosidase) (EC 3.2.2.22).			
OS	Phytolacca americana (Common pokeweed) (Virginia pokeweed).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Phytolaccaceae; Phytolacca.			
OC	NCBI_TaxID=3527;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Seed, Leaf, and root;			
RX	MEDLINE=9309240; PubMed=1281438;			
RA	Kataoka J., Habuka N., Masuta C., Miyano M., Koizumi A.,			
RT	"Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein.";			
RL	Plant Mol. Biol. 20:879-886(1992).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).			
RX	MEDLINE=95010127; PubMed=7925458;			
RA	Ago H., Kataoka J., Tsuge H., Nakaba N., Inagaki E., Noma M.,			

FT	HELIX	164	174
FT	TURN	175	176
FT	HELIX	182	195
FT	TURN	196	196
FT	HELIX	197	201
FT	HELIX	203	211
FT	TURN	212	214
FT	STRAND	217	217
FT	STRAND	221	239
FT	HELIX	241	241
FT	TURN	242	243
FT	STRAND	244	252
FT	TURN	254	255
FT	STRAND	258	263
FT	HELIX	264	270
FT	STRAND	274	274
SQ	SEQUENCE	313 AA:	35219 MW: 265702861EBA57F5 CRC64:

Query Match 76.4% Score 1235.5; DB 1: Length 313;
Best Local Similarity 75.9%; Pred. No. 4.9e-91;
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;

QY	1	MKVMLVVVVTLLIHLIAAPTSTCAINTITFDAGNATINKYATPESLRNOAKDPKIKCYG	60
DB	1	MSMLVVTISI--WLLAPTSTMAVNTIYVGVSTTISKYATFLNDLRNEAKDPSIKCYG	58
QY	61	IPMLPOTNTPKYLVLKQGANLKTITLMRLNNLYVMGYSDPFNGKCRVHIFNDIEST	120
DB	59	IPMLPNTNPKYVLVLEQGSNKKVITLMRLNNLYVMGYSDPFNPKCRVHIFNDISCT	118
QY	121	ERTDVENTLCSSSSSKVAMSNYNSLYPTMEKKAEVNSRNOVOLGIGIQICLSIDGKICWD	180
DB	119	ERQDVETTLCPNANSRVSKNINFDSPRTLESKAGVSRQVQLGILDSNIGKISGM	178
QY	181	SPVKTAEFFLLVQVMVSEAAKPKYIENOVKTNFNPAYPDPKVINLEEKWKISEAH	240
DB	179	SFVKTAEFFLLVQVMVSEAAKPKYIENOVKTNFNPAYPDPKVINLEEKWKISEAH	238
QY	241	NAKNGALPKPLVDKAGTKTWILRVDEINRDVALLKYVNGTCQTTY-QNAMFSQVILST	299
DB	239	DAKNGVLPKPLVDASGAKWILRVKDELKPDVALLVYVGGSCQTTYQNAFPOIINST	298
QY	300	YNNYMSNLGDLLEEGF	314
DB	299	YNNYMNVLGDLLEEGF	313

GenCore version 5.1.4_p5.4578
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protein - protein search, using sw model

Run on: May 28, 2003, 09:46:19 ; Search time 25 seconds
(without alignments)
520.943 Million cell updates/sec

Title: US-09-978-274A-2
Perfect score: 1617
Sequence: 1 MKVHLVVVTLIAALIAAPT.....VLIITYYNSNGLDFEGF 314

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query Match	Length	ID	Description
1	1235.5	76.4	313	1 RIPL_PHYAM	P10297 phytolacca
2	1113.5	68.9	294	1 RIPA_PHYAM	Q03464 phytolacca
3	1096.5	67.8	261	1 RIPS_PHYAM	P23339 phytolacca
4	511	31.6	310	1 RIPL_PHYAM	Q40772 phytolacca
5	378.5	23.4	299	1 RIPA_PHYAM	P20656 saponaria o
6	372	23.0	292	1 RIPL_PHYAM	P27559 saponaria o
7	345.5	21.4	293	1 RIPO_PHYAM	P24476 dianthus ca
8	337	20.8	253	1 RIPL_PHYAM	Q41389 saponaria o
9	336	20.8	253	1 RIPL_PHYAM	Q41391 saponaria o
10	330	20.4	316	1 RIPL_PHYAM	P33186 gelonium mu
11	305.5	18.9	576	1 RIPL_PHYAM	P2879 ricinus com
12	300	18.6	294	1 RIPL_PHYAM	P56626 trichosanthe
13	285	17.6	236	1 RIPL_PHYAM	P27560 saponaria o
14	279.5	17.3	278	1 RIPL_PHYAM	P13326 marabalis j
15	271.5	16.8	564	1 RIPL_PHYAM	P6750 ricinus com
16	263	16.3	282	1 RIPL_PHYAM	P8184 bryonia dio
17	253	15.6	286	1 RIPL_PHYAM	Q91x4 cucumis fig
18	249.5	15.4	286	1 RIPL_PHYAM	P16094 momordica c
19	246	15.2	289	1 RIPL_PHYAM	P09989 trichosanthe
20	245.5	15.2	289	1 RIPL_PHYAM	P24478 trichosanthe
21	238.5	14.7	563	1 RIPL_PHYAM	P33183 sambucus ni
22	236.5	14.6	286	1 RIPL_PHYAM	P29339 momordica b
23	235	14.5	250	1 RIPL_PHYAM	P22851 luffa cylin
24	232.5	14.4	290	1 RIPL_PHYAM	P33185 bryonia dio
25	232.5	14.4	528	1 RIPL_PHYAM	P11140 abrus preca
26	231	14.3	527	1 RIPL_PHYAM	Q06077 abrus preca
27	227	14.0	562	1 RIPL_PHYAM	P28590 abrus preca
28	207	12.8	277	1 RIPL_PHYAM	Q00465 luffa cylin
29	202	12.5	157	1 RIPL_PHYAM	P27561 saponaria o
30	200	12.4	254	1 RIPL_PHYAM	P81446 viscum albu
31	131	8.1	32	1 RIPL_PHYAM	P34967 phytolacca
32	130.5	8.1	315	1 RIPL_PHYAM	P08026 bacterioph
33	127.5	7.9	315	1 RIPL_PHYAM	P10149 bacterioph

34	121	7.5	315	1 SLTA_00933	P09385 bacterioph
35	119	7.4	300	1 RIPL_PHYAM	P25891 zeamays (m
36	112.5	7.0	280	1 RIPL_PHYAM	P04399 hordeum vul
37	111.5	6.9	560	1 RIPL_PHYAM	Q00531 hordeum vul
38	111	6.9	3343	1 YOG7_CAPEL	P34616 caenorhabd1
39	109.5	6.8	280	1 RIPL_PHYAM	P22244 hordeum vul
40	105.5	6.5	301	1 RIPL_PHYAM	P28522 zeamays (m
41	103	6.4	304	1 RIPL_PHYAM	P25892 zeamays (m
42	97.5	6.0	485	1 HXKA_YEAST	P04806 saccharomyc
43	94.5	5.8	385	1 GBAS_CAPEL	Q20701 saccharomyc
44	92.5	5.7	303	1 RIPL_PHYAM	P10593 zeamays (m
45	92.5	5.7	484	1 YA62_METJA	Q58462 methanococc

ALIGNMENTS

RESULT 1	RIPL_PHYAM	STANDARD:	PRT:	313 AA.
AC	P10297			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Antiviral protein I precursor (PAP-I) (PAP-C) (Ribosome-inactivating protein) (rRNA N-glycosidase) (EC 3.2.2.22).			
DE	PAP-I			
GN	Phytolacca americana (Common pokeweed) (Virginian pokeweed).			
OS	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.			
OX	NCBI_TaxID=3527;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 23-62.			
RC	TISSUE=Leaf;			
RC	MEDLINE=92003676; PubMed=1912488;			
RA	Lin Q., Chen Z.C., Antoniw J.F., White R.F.;			
KT	"Isolation and characterization of a cDNA clone encoding the anti-viral protein from Phytolacca americana.";			
RT	Plant Mol. Biol. 17:609-614(1991).			
RL	[2]			
RP	SEQUENCE OF 23-65.			
RC	MEDLINE=89193489; PubMed=2930487;			
RA	Barbieri L., Bolognesi A., Ceini P., Falasca A.I., Minghetti A.,			
RA	Garofano L., Guicciardi A., Lepel D., Miller S.P.;			
RT	"Ribosome-inactivating proteins from plant cells in culture.";			
RL	Biochem. J. 257:801-807(1989).			
RC	[3]			
RP	SEQUENCE OF 23-54.			
RC	TISSUE=Leaf;			
RC	MEDLINE=83290867; PubMed=6885760;			
RA	Houston L., Ramakrishnan S., Hermodson M.A.;			
RT	"Seasonal variations in different forms of pokeweed antiviral protein, a potent inactivator of ribosomes.";			
RL	J. Biol. Chem. 258:9601-9604(1983).			
RC	[4]			
RP	SEQUENCE OF 23-54.			
RC	TISSUE=Leaf;			
RC	MEDLINE=85023392; PubMed=6091760;			
RA	Bjorn M.J., Larrick J., Platak M., Wilson K.J.;			
RT	"Characterization of translational inhibitors from Phytolacca americana: amino-terminal sequence determination and antibody-inhibitor conjugates.";			
RL	Biochim. Biophys. Acta 790:154-163(1984).			
RC	[5]			
RP	SEQUENCE OF 23-54.			
RC	TISSUE=Root;			
RC	MEDLINE=91064383; PubMed=2248976;			
RA	Bolognesi A., Barbieri L., Abbondanza A., Falasca A.I., Carnicelli D.,			
RA	Battelli M.G., Shirone F.;			
RT	"Purification and properties of new ribosome-inactivating proteins with RNA N-glycosidase activity.";			
RL	Biochim. Biophys. Acta 1087:293-302(1990).			

Query Match 2.5%; Score 8; DB 1; Length 328;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 212 KTNFNRA 219
 |||||
 60 KTNFNRA 67

RESULT 14
 B86600
 D-alanine/glycine permease [Imported] - Chlamydomonas reinhardtii (strain J138)
 C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: B86600
 R:Shirai, M.; Hiraoka, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishii, Y.
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: B86600
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-458 <STO>
 A:Cross-references: GB:BA000008; MID:98979250; PIDN:BAA99084.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: daqA_2
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 2.5%; Score 8; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 270 NR0VALK 277
 |||||
 436 NR0VALK 443

RESULT 15
 B72024
 d-alanine/glycine permease - Chlamydomonas reinhardtii (strain CWL029)
 C:Species: Chlamydomonas reinhardtii, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 C:Accession: B72024
 R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: B72024
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-458 <ARN>
 A:Cross-references: GB:AE001363; MID:94377192; PIDN:AAD19014.1; PID:9437719
 A:Experimental source: strain CWL029
 C:Genetics:
 A:Gene: daqA_2
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 2.5%; Score 8; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 270 NR0VALK 277
 |||||
 436 NR0VALK 443

Search completed: May 28, 2003, 10:12:40
 Time: 47 secs

Printed 11/17/2004

Submitted to the Brookhaven Protein Data Bank, July 1994
 Reference number: A67089; PDB:1MRH
 Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77, 'R', 79-132.
 Function:
 Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA that
 Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 Keywords: glycoprotein; glycosidase; hydrolase; lectin; seed; toxin
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-23/Domain: amino-terminal propeptide #status predicted <PRO>
 F:24-269/Product: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>
 F:27-286/Domain: rRNA N-glycosidase homology <RNG>
 F:270-286/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:93,183,186/Active site: Tyr, Glu, Arg #status predicted
 F:250/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 2.9% Score 9; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 EAARFKYIE 208
 I I I I I I I I I I
 DB 183 EAARFKYIE 191

RESULT 10

S25560
 rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple
 C:Species: Momordica balsamina (balsam apple)
 C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999
 C:Accession: S25560
 R:Ortigao, M.; Better, M.
 Nucleic Acids Res. 20, 4662, 1992
 Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homologous to the N-glycosidase from Momordica charantia
 Reference number: S25560; MUID: 93027170; PMID:1408771
 Accession: S25560
 Status: preliminary
 Molecule type: mRNA
 Residues: 1-286 <ORT>
 A:Cross-references: EMBL:212175; NID:g19525; PDB:CAA78166.1; PTD:g19526
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C:Keywords: glycosidase; hydrolase
 F:27-286/Domain: rRNA N-glycosidase homology <RNG>

Query Match 2.9% Score 9; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 EAARFKYIE 208
 I I I I I I I I I I
 DB 181 EAARFKYIE 189

RESULT 11

T32320
 hypothetical protein C41H7.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T32320
 R:Giesel, C.; Wamsley, P.; Elliott, G.; Smith, A.
 Submitted to the EMBL Data Library, September 1997
 Description: The sequence of C. elegans cosmid C41H7.
 Reference number: 221150
 Accession: T32320
 Status: preliminary; translated from GB/EMBL/DBJ
 Molecule type: DNA
 Residues: 1-321 <GEI>

A:Cross-references: EMBL:AF025450; PDB:AAB70937.1; GSPDB:GN00020; CESP:C41H7.6
 A:Experimental source: strain Bristol N2; clone C41H7
 A:Genetics:
 A:Gene: CESP:C41H7.6
 A:Map position: 2
 A:Introns: 93/1; 183/2
 Superfamily: Caenorhabditis elegans hypothetical protein C08A9.6

Query Match 2.5% Score 8; DB 2; Length 321;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 SNLGDLE 312
 I I I I I I I I I I
 DB 294 SNLGDLE 301

RESULT 12

T32321
 hypothetical protein C41H7.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T32321
 R:Giesel, C.; Wamsley, P.; Elliott, G.; Smith, A.
 Submitted to the EMBL Data Library, September 1997
 Description: The sequence of C. elegans cosmid C41H7.
 Reference number: 221150
 Accession: T32321
 Status: preliminary; translated from GB/EMBL/DBJ
 Molecule type: DNA
 Residues: 1-327 <GEI>
 A:Cross-references: EMBL:AF025450; PDB:AAB70936.1; GSPDB:GN00020; CESP:C41H7.5
 A:Experimental source: strain Bristol N2; clone C41H7
 C:Genetics:
 A:Gene: CESP:C41H7.5
 A:Map position: 2
 A:Introns: 99/1; 189/2
 C:Superfamily: Caenorhabditis elegans hypothetical protein C08A9.6

Query Match 2.5% Score 8; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 SNLGDLE 312
 I I I I I I I I I I
 DB 300 SNLGDLE 307

RESULT 13

C70039
 two-component sensor histidine kinase homolog yvfr - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: C70039
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber
 C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;
 A.: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fahnestock, G.; Ferrati,
 Nature 390, 249-256, 1997
 Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidos, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y., M.; Ogawa, K.; Ogawa, A.; Oudejans, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porcete
 Rieger, M.; Kivolta, C.; Kocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scani
 A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Toyonari, A.; Tsubota, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zumbstein, E.; Yoshikawa, H.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 Accession: C70039
 Status: preliminary; nucleic acid sequence not shown; translation not shown
 Molecule type: DNA
 Residues: 1-328 <KUN>
 A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PDB:CAE15412.1; PTD:g26359
 A:Experimental source: strain 168
 A:Genetics:
 A:Gene: yvfr
 C:Superfamily: probable Bacillus subtilis two-component sensor histidine kinase yocF

Accession: S62627; S62619
R:van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.
Eur. J. Biochem. 235, 128-137, 1996
A:Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (*Sambucus nigra*)
A:Reference number: S62619; MUID:96202926; PMID:8631319
A:Accession: S62627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <VA>
A:Cross-references: EMBL:U27122; NID:gl141772; PIDN:AAC49158.1; PID:gl141773
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-39; 309-319 <VA2>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:37-283/Domain: rRNA N-glycosidase homology <RNG>
Query Match 3.2%; Score 10; DR 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 IOMVSEARF 204
DB 194 IOMVSEARF 203
RESULT 9
RUPUGG
rRNA N-glycosidase (EC 3.2.2.22) alpha-momorcharin precursor (validated) - balsam pear
A:Alternate names: agglutinin; momordin-A; ribosome-inactivating protein momorcharin
C:Species: Momordica charantia (balsam pear, bitter melon)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 15-Sep-2000
A:Accession: S14273; A61318; S16490; JN0628; S01670
R:Ho, W.K.K.; Liu, S.C.; Shaw, P.C.; Feung, H.W.; Ng, T.B.; Chau, W.Y.
Biochim. Biophys. Acta 1088, 311-314, 1991
A:Title: Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein.
A:Reference number: S14273; MUID:91159486; PMID:2001404
A:Accession: S14273
A:Molecule type: mRNA
A:Residues: 1-286 <HOM>
A:Cross-references: EMBL:X57682; NID:gl9527; PIDN:CAA40869.1; PID:gl9528
R:Li, S.S.L.
Experientia 36, 524-527, 1980
A:Title: Purification and partial characterization of two lectins from Momordica charantia
A:Reference number: A61318; MUID:80201763; PMID:7379938
A:Accession: A61318
A:Molecule type: protein
A:Residues: 24-50 <LIA>
A>Note: as a lectin shows agglutinating activity for type-O red blood cells
R:Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Sorio, M.; Lippi, D.
Int. J. Pept. Protein Res. 33, 263-267, 1989
A:Title: N-terminal sequence of some ribosome-inactivating proteins.
A:Reference number: S16331; MUID:89326691; PMID:2753596
A:Accession: S16490
A:Molecule type: protein
A:Residues: 24-68, 'X', 70 <MON>
R:Minami, Y.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 1141-1144, 1993
A:Title: The complete amino acid sequence of momordin-a, a ribosome-inactivating protein
A:Reference number: JN0628; MUID:93372485; PMID:7763984
A:Accession: JN0628
A:Molecule type: protein
A:Residues: 24-107, 'O', 109-123, 125-147, 'L', 149-154, 'I', 156-205, 'I', 207-208, 'L', 210-211, 'D', 212-213, 'D', 214-215, 'D', 216-217, 'D', 218-219, 'D', 220-221, 'D', 222-223, 'D', 224-225, 'D', 226-227, 'D', 228-229, 'D', 230-231, 'D', 232-233, 'D', 234-235, 'D', 236-237, 'D', 238-239, 'D', 240-241, 'D', 242-243, 'D', 244-245, 'D', 246-247, 'D', 248-249, 'D', 250-251, 'D', 252-253, 'D', 254-255, 'D', 256-257, 'D', 258-259, 'D', 260-261, 'D', 262-263, 'D', 264-265, 'D', 266-267, 'D', 268-269, 'D', 270-271, 'D', 272-273, 'D', 274-275, 'D', 276-277, 'D', 278-279, 'D', 280-281, 'D', 282-283, 'D', 284-285, 'D', 286-287, 'D', 288-289, 'D', 290-291, 'D', 292-293, 'D', 294-295, 'D', 296-297, 'D', 298-299, 'D', 300-301, 'D', 302-303, 'D', 304-305, 'D', 306-307, 'D', 308-309, 'D', 310-311, 'D', 312-313, 'D', 314-315, 'D', 316-317, 'D', 318-319, 'D', 320-321, 'D', 322-323, 'D', 324-325, 'D', 326-327, 'D', 328-329, 'D', 330-331, 'D', 332-333, 'D', 334-335, 'D', 336-337, 'D', 338-339, 'D', 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Cross-references: EMDL:D10569

00 Z1 ESRNQAUP 30

GenCore version 5.1.4.p5.4578
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protein - protein search, using sw model

Run on: May 28, 2003, 10:07:20 ; Search time 46 Seconds
(without alignments)
656.222 Million cell updates/sec

Title: US-09-978-274A-2
Perfect score: 314
Sequence: 1 MKVMLVVVVTLLAWLIAAPT.....VIISTYYNYSNGLDLEFC 314

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 segs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	10.2	294	2 S28421	rRNA N-glycosidase
2	30	9.6	313	2 S17757	rRNA N-glycosidase
3	28	8.9	261	2 JE0401	antiviral protein
4	14	4.5	278	2 A39817	rRNA N-glycosidase
5	10	3.2	32	2 S38528	rRNA N-glycosidase
6	10	3.2	106	2 S39761	abrin (clone 3.7)
7	10	3.2	316	2 JT0753	rRNA N-glycosidase
8	10	3.2	570	2 S62627	agglutinin I precu
9	9	2.9	286	1 RLPUGG	rRNA N-glycosidase
10	9	2.9	286	2 S25560	rRNA N-glycosidase
11	8	2.5	321	2 T32320	hypothetical prote
12	8	2.5	327	2 T32321	hypothetical prote
13	8	2.5	328	1 C70039	two-component sens
14	8	2.5	458	2 B86600	D-alanine/glycine
15	8	2.5	458	2 B72024	D-alanine/glycine
16	8	2.5	588	2 T24121	hypothetical prote
17	8	2.5	1539	2 T48059	ABC transporter-li
18	7	2.2	68	2 E90320	hypothetical prote
19	7	2.2	92	2 C40358	hypothetical prote
20	7	2.2	123	2 S67584	probable membrane
21	7	2.2	133	2 T21739	hypothetical prote
22	7	2.2	132	1 RWM5A3	T-cell receptor al
23	7	2.2	142	2 S38390	T-cell receptor be
24	7	2.2	144	2 A27577	T-cell receptor al
25	7	2.2	149	2 T47597	hypothetical prote
26	7	2.2	175	2 B72632	hypothetical prote
27	7	2.2	193	2 AF1981	hypothetical prote
28	7	2.2	217	2 H72391	dihydroorotate deh
29	7	2.2	220	2 A12182	hypothetical prote

hypothetical prote
orf 5' to uraA - M
hypothetical prote
betaverrin - beet
factor IX - rabbit
conjugation factor
pyridoxal/pyridoxi
pyridoxal/pyridoxi
rRNA N-glycosidase
rRNA N-glycosidase
hypothetical prote
TPR-repeat-contain
ribosome-inactivat
acetylcholinesterase
oligopeptide ABC t
hypothetical prote

ALIGNMENTS

RESULT 1

S28421
rRNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed
N:Alternate names: antiviral protein alpha-PAP
C:Species: Phytolacca americana (Virginian pokeweed)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C:Accession: S28421

R:Katoaka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koizumi, A.
Plant Mol. Biol. 20, 879-886, 1992

A:Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein

A:Reference number: S28421; MUID:93059240; PMID:1281438

A:Accession: S28421

A:Molecule type: DNA

A:Residues: 1-294 <RAT>

A:Cross-references: EMBL:D10600; NID:g218010; PIDN:RAA01451.1; PID:g218011

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase

F:30-278/Domain: rRNA N-glycosidase homology <RNG>

Query Match 10.2% Score 32: DB 2: Length 294;

Best Local Similarity 100.0%; Pred. No. 5.5e-24;

Matches 32: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 190 FLVAIVMVSEAAKFYIENQVKTENFRAEYP 221

|||||

DB 189 FLVAIVMVSEAAKFYIENQVKTENFRAEYP 220

RESULT 2

S17757

rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed

N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-

C:Species: Phytolacca americana (Virginian pokeweed)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999

C:Accession: S17757; S02792; S13469; S32611

R:Lin, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.

Plant Mol. Biol. 17, 609-614, 1991

A:Title: Isolation and characterization of a cDNA clone encoding the anti-viral prote

A:Reference number: S17757; MUID:92003676; PMID:1912488

A:Accession: S17757

A:Molecule type: RNA

A:Residues: 1-313 <LIN>

A:Cross-references: EMBL:X55383; NID:g20421; PIDN:CAA39054.1; PID:g20422

R:Barbieri, L.; Bolonnesi, A.; Gemini, P.; Falasca, A.I.; Minchetti, A.; Garofano, L.

Biochem. J. 257, 801-807, 1989

A:Title: Ribosome-inactivating proteins from plant cells in culture.

A:Reference number: S02792; MUID:89134489; PMID:2930487

A:Accession: S02792

A:Molecule type: protein

A:Residues: 23-55, 'X', 57-65 <BAR>

R:Bolonnesi, A.; Barbieri, L.; Abundanza, A.; Falasca, A.I.; Carnicelli, D.; Battelli

Biochim. Biophys. Acta 1087, 293-302, 1990

processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a Type I ribosomal inhibitor protein (RIP) that catalyzes the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without causing plant cell death or sterility. They can also confer increased resistance to insects, bacteria and nematodes in plants. N.B. This sequence is not given in the specification but is generated from the wild type sequence reproduced in the specification.

Sequence 207 AA:
Query Match 9.6%; Score 30; DB 18; Length 207;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

190 FLVATQMVSEARFKYIENQVKTNFRAF 219
166 FLVATQMVSEARFKYIENQVKTNFRAF 195

RESULT 15

AAW14193
O AAW14193 standard: protein; 208 AA.

AAW14193;

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-208).

Pokeweed antiviral protein; mutant: phytotoxicity; anti-viral; virus; anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect; stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding; translation; broad spectrum; resistance; cell death; sterility; nematode; bacterium.

Phytolacca americana.

W09703183-A1.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Tuner NE;

WPI; 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral and anti-fungal activity in plants and have reduced phytotoxicity

Claim 8; 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytotoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a Type I ribosomal inhibitor protein (RIP) that catalyzes the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can

CC confer broad spectrum virus and fungus resistance to plants without causing plant cell death or sterility. They can also confer increased resistance to insects, bacteria and nematodes in plants. N.B. This sequence is not given in the specification but is generated from the wild type sequence reproduced in the specification.

XX Sequence 208 AA;

Query Match 9.6%; Score 30; DB 18; Length 208;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 FLVATQMVSEARFKYIENQVKTNFRAF 219
DB 166 FLVATQMVSEARFKYIENQVKTNFRAF 195

Search completed: May 28, 2003, 10:09:42
Job time : 78 secs

New pokeweed antiviral protein mutants - which exhibit anti-viral and anti-fungal activity in plants and have reduced phytotoxicity

Claim 8: - 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytotoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a type I ribosomal inhibitor protein (RIP) that catalyses the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without causing plant cell death or sterility. They can also confer increased resistance to insects, bacteria and nematodes in plants. N.B. This sequence is not given in the specification but is generated from the wild type sequence reproduced in the specification.

Sequence 205 AA:

Query Match 9.6%; Score 30; DB 18; Length 205;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

190 FLVATQMVSEAAARFYIENQVKTNFRAF 219
|||||
166 FLVATQMVSEAAARFYIENQVKTNFRAF 195

13
195

AAW14195 standard; protein; 206 AA.

AAW14195;

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-206).

Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus; anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect; stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding; translation; broad spectrum; resistance; cell death; sterility; nematode; bacterium.

Phytolacca americana.

WO9703183-A1.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTE) UNIV RUTGERS STATE NEW JERSEY.

Turner NE;

WPI: 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral and anti-fungal activity in plants and have reduced phytotoxicity

Claim 8: - 64pp; English.

06/02/2003

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytotoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a type I ribosomal inhibitor protein (RIP) that catalyses the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without causing plant cell death or sterility. They can also confer increased resistance to insects, bacteria and nematodes in plants. N.B. This sequence is not given in the specification but is generated from the wild type sequence reproduced in the specification.

XX Sequence 206 AA:

Query Match 9.6%; Score 30; DB 18; Length 206;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

190 FLVATQMVSEAAARFYIENQVKTNFRAF 219
|||||
166 FLVATQMVSEAAARFYIENQVKTNFRAF 195

RESULT 14

AAW14194

ID AAW14194 standard; protein; 207 AA.

AC AAW14194;

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-207).

Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus; anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect; stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding; translation; broad spectrum; resistance; cell death; sterility; nematode; bacterium.

Phytolacca americana.

WO9703183-A1.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTE) UNIV RUTGERS STATE NEW JERSEY.

Turner NE;

WPI: 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral and anti-fungal activity in plants and have reduced phytotoxicity

Claim 8: - 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytotoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to

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30-JAN-1997.
11-JUL-1996; 96WO-US11546.
11-JUL-1995; 95US-0500694.
11-JUL-1995; 95US-0500611.
(RUTF ) UNIV RUTGERS STATE NEW JERSEY.
Tuner NE:
WPI: 1997-119040/11.
New pokeweed antiviral protein mutants - which exhibit anti-viral
and anti-fungal activity in plants and have reduced phytotoxicity
Claim 8: -: 64pp: English.
Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
mutants having reduced phytotoxicity but retaining anti-viral or
anti-fungal activity in plants. The sequences, numbering corresponds to
the 262 amino acid mature protein. The proteins AAW14165-W14217
represent serial deletions from the C-terminus whereas sequences
AAW14218-55 are serial deletions from the N-terminus. Prior to
processing, the protein contains a 22 amino acid N-terminal signal
sequence and a 29 amino acid C-terminal extension. PAP is a Type I
ribosomal inhibitor protein (RIP) that catalyses the removal of a
specific adenine residue from a highly conserved stem-loop structure in
the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
factor-2 binding thus blocking protein translation. The PAP mutants can
confer broad spectrum virus and fungus resistance to plants without
causing plant cell death or sterility. They can also confer increased
resistance to insects, bacteria and nematodes in plants.
N.B. This sequence is not given in the specification but is generated
from the wild type sequence reproduced in the specification.
Sequence 203 AA:
Query Match 9.6%; Score 30; DB 18; Length 203;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 190 FLVAIQMVSEAAAREKYIENQVKTNFRAF 219
DDB 166 FLVAIQMVSEAAAREKYIENQVKTNFRAF 195
RESULT 11
AAW14197
AAW14197 standard; protein; 204 AA.
AAW14197;
25-JUN-1997 (first entry)
Mature pokeweed antiviral protein deletion variant (1-204).
Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
translation; broad spectrum; resistance; cell death; sterility; nematode;
bacterium.
Phytolacca americana.
WO9703183-A1.
30-JAN-1997.
11-JUL-1996; 96WO-US11546.
11-JUL-1995; 95US-0500694.
11-JUL-1995; 95US-0500611.
(RUTF ) UNIV RUTGERS STATE NEW JERSEY.
Tuner NE:
WPI: 1997-119040/11.
New pokeweed antiviral protein mutants - which exhibit anti-viral
and anti-fungal activity in plants and have reduced phytotoxicity
Claim 8: -: 64pp: English.
Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
mutants having reduced phytotoxicity but retaining anti-viral or
anti-fungal activity in plants. The sequences, numbering corresponds to
the 262 amino acid mature protein. The proteins AAW14165-W14217
represent serial deletions from the C-terminus whereas sequences
AAW14218-55 are serial deletions from the N-terminus. Prior to
processing, the protein contains a 22 amino acid N-terminal signal
sequence and a 29 amino acid C-terminal extension. PAP is a Type I
ribosomal inhibitor protein (RIP) that catalyses the removal of a
specific adenine residue from a highly conserved stem-loop structure in
the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
factor-2 binding thus blocking protein translation. The PAP mutants can
confer broad spectrum virus and fungus resistance to plants without
causing plant cell death or sterility. They can also confer increased
resistance to insects, bacteria and nematodes in plants.
N.B. This sequence is not given in the specification but is generated
from the wild type sequence reproduced in the specification.
Sequence 204 AA:
Query Match 9.6%; Score 30; DB 18; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 190 FLVAIQMVSEAAAREKYIENQVKTNFRAF 219
DDB 166 FLVAIQMVSEAAAREKYIENQVKTNFRAF 195
RESULT 12
AAW14196
AAW14196 standard; protein; 205 AA.
AAW14196;
25-JUN-1997 (first entry)
Mature pokeweed antiviral protein deletion variant (1-205).
Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
translation; broad spectrum; resistance; cell death; sterility; nematode;
bacterium.
Phytolacca americana.
WO9703183-A1.
30-JAN-1997.
11-JUL-1996; 96WO-US11546.
11-JUL-1995; 95US-0500694.
11-JUL-1995; 95US-0500611.
(RUTF ) UNIV RUTGERS STATE NEW JERSEY.
Tuner NE:
WPI: 1997-119040/11.

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Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus; anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect; stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding; translation; broad spectrum; resistance; cell death; sterility; nematode;

WO9703183-A1.

|||||
166 FLVIAQMVSAAAEKYIENQVKTENRAF 195

RESULT 6

AAW14202

ID AAW14202 standard; protein: 199 AA.

AAW14202:

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-199).

Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
translation; broad spectrum; resistance; cell death; sterility; nematode;
bacterium.

Phytolacca americana.

WO9703183-Al.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Tumor NE;

WPI: 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral
and anti-fungal activity in plants and have reduced phytotoxicity

Claim 8: -; 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
mutants having reduced phytotoxicity but retaining anti-viral or
anti-fungal activity in plants. The sequences' numbering corresponds to
the 262 amino acid mature protein. The proteins AAW14163-W14217
represent serial deletions from the C-terminus whereas sequences
AAW14218-55 are serial deletions from the N-terminus. Prior to
processing, the protein contains a 22 amino acid N-terminal signal
sequence and a 29 amino acid C-terminal extension. PAP is a Type I
ribosomal inhibitor protein (RIP) that catalyses the removal of a
specific adenine residue from a highly conserved stem-loop structure in
the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
factor-2 binding thus blocking protein translation. The PAP mutants can
confer broad spectrum virus and fungus resistance to plants without
causing plant cell death or sterility. They can also confer increased
resistance to insects, bacteria and nematodes in plants.
N.B. This sequence is not given in the specification but is generated
from the wild type sequence reproduced in the specification.

Sequence 199 AA:

Query Match 9.6%; Score 30; DB 18; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

190 FLVIAQMVSAAAEKYIENQVKTENRAF 219

166 FLVIAQMVSAAAEKYIENQVKTENRAF 195

RESULT 7

AAW14201

ID AAW14201 standard; protein: 200 AA.

AAW14201:

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-200).

Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
translation; broad spectrum; resistance; cell death; sterility; nematode;
bacterium.

Phytolacca americana.

WO9703183-Al.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Tumor NE;

WPI: 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral
and anti-fungal activity in plants and have reduced phytotoxicity

Claim 8: -; 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
mutants having reduced phytotoxicity but retaining anti-viral or
anti-fungal activity in plants. The sequences' numbering corresponds to
the 262 amino acid mature protein. The proteins AAW14163-W14217
represent serial deletions from the C-terminus whereas sequences
AAW14218-55 are serial deletions from the N-terminus. Prior to
processing, the protein contains a 22 amino acid N-terminal signal
sequence and a 29 amino acid C-terminal extension. PAP is a Type I
ribosomal inhibitor protein (RIP) that catalyses the removal of a
specific adenine residue from a highly conserved stem-loop structure in
the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
factor-2 binding thus blocking protein translation. The PAP mutants can
confer broad spectrum virus and fungus resistance to plants without
causing plant cell death or sterility. They can also confer increased
resistance to insects, bacteria and nematodes in plants.
N.B. This sequence is not given in the specification but is generated
from the wild type sequence reproduced in the specification.

Sequence 200 AA:

Query Match 9.6%; Score 30; DB 18; Length 200;

Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 FLVIAQMVSAAAEKYIENQVKTENRAF 219

166 FLVIAQMVSAAAEKYIENQVKTENRAF 195

RESULT 8

AAW14200

ID AAW14200 standard; protein: 201 AA.

AAW14200:

25-JUN-1997 (first entry)

New pokeweed antiviral protein (PAP) with similar activity to ricin - used to treat cancer and as an agricultural chemical

Claim 1: Page 11-13; 14pp; Japanese.

NB: A protein comprising 261 amino acids is claimed. PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The protein may be obtained all year round by recombinant DNA techniques. PAP can be used partic. against cancer and as an agricultural chemical.

Total mRNA is extracted from the seeds, leaves and roots of pokeweed and used to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA fractions, which are introduced into a cloning vector EMBL3 and then into host E.coli PLK-17 (P2) to produce PAP.

Query Match 10.2%; Score 32; DB 14; Length 294;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

190 FLVAIQMVSEAAAREKYIENQVKTNFNRAFP 221
189 FLVAIQMVSEAAAREKYIENQVKTNFNRAFP 220

RESULT 2
ID AAW14206 standard; protein: 195 AA.

XX AAW14206;

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-195).

Pokeweed antiviral protein; mutant; phytoxicity: anti-viral; virus; anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect; stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding; translation; broad spectrum; resistance; cell death; sterility; nematode; bacterium.

Phytolacca americana.

WO9703183-A1.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Tuner NE;

WPI: 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral and anti-fungal activity in plants and have reduced phytoxicity

Claim 8: -; 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to processing, the protein contains a 22 amino acid N-terminal signal

sequence and a 29 amino acid C-terminal extension. PAP is a Type I ribosomal inhibitor protein (RIP) that catalyses the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without causing plant cell death or sterility. They can also confer increased resistance to insects, bacteria and nematodes in plants. N.B. This sequence is not given in the specification but is generated from the wild type sequence reproduced in the specification.

Sequence 195 AA;

Query Match 9.6%; Score 30; DB 18; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

190 FLVAIQMVSEAAAREKYIENQVKTNFNRAF 219
166 FLVAIQMVSEAAAREKYIENQVKTNFNRAF 195

RESULT 3

AAW14205

ID AAW14205 standard; protein: 196 AA.

XX AAW14205;

25-JUN-1997 (first entry)

Mature pokeweed antiviral protein deletion variant (1-196).

Pokeweed antiviral protein; mutant; phytoxicity: anti-viral; virus; anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect; stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding; translation; broad spectrum; resistance; cell death; sterility; nematode; bacterium.

Phytolacca americana.

WO9703183-A1.

30-JAN-1997.

11-JUL-1996; 96WO-US11546.

11-JUL-1995; 95US-0500694.

11-JUL-1995; 95US-0500611.

(RUTF) UNIV RUTGERS STATE NEW JERSEY.

Tuner NE;

WPI: 1997-119040/11.

New pokeweed antiviral protein mutants - which exhibit anti-viral and anti-fungal activity in plants and have reduced phytoxicity

Claim 8: -; 64pp; English.

Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP) mutants having reduced phytoxicity but retaining anti-viral or anti-fungal activity in plants. The sequences' numbering corresponds to the 262 amino acid mature protein. The proteins AAW14165-W14217 represent serial deletions from the C-terminus whereas sequences AAW14218-55 are serial deletions from the N-terminus. Prior to processing, the protein contains a 22 amino acid N-terminal signal sequence and a 29 amino acid C-terminal extension. PAP is a Type I ribosomal inhibitor protein (RIP) that catalyses the removal of a specific adenine residue from a highly conserved stem-loop structure in the 28S rRNA of eukaryotic ribosomes and also interferes with elongation factor-2 binding thus blocking protein translation. The PAP mutants can confer broad spectrum virus and fungus resistance to plants without

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protein - protein search, using sw model

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(without alignments)
543.386 Million cell updates/sec

Title: US-09-978-274A-2
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Gapop 60.0 , Capext 60.0

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ord size : 0

total number of hits satisfying chosen parameters: 908470

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID	Score	Query Match	Length	DB	Description
1	32	10.2	294	14	AA837345 Pokeweed antiviral
2	30	9.6	195	18	AAW14206 Mature pokeweed an
3	30	9.6	196	18	AAW14205 Mature pokeweed an
4	30	9.6	197	18	AAW14204 Mature pokeweed an
5	30	9.6	198	18	AAW14203 Mature pokeweed an
6	30	9.6	199	18	AAW14202 Mature pokeweed an
7	30	9.6	200	18	AAW14201 Mature pokeweed an
8	30	9.6	201	18	AAW14200 Mature pokeweed an
9	30	9.6	202	18	AAW14199 Mature pokeweed an
10	30	9.6	203	18	AAW14198 Mature pokeweed an

11	30	9.6	204	18	AAW14197 Mature pokeweed an
12	30	9.6	205	18	AAW14196 Mature pokeweed an
13	30	9.6	206	18	AAW14195 Mature pokeweed an
14	30	9.6	207	18	AAW14194 Mature pokeweed an
15	30	9.6	208	18	AAW14193 Mature pokeweed an
16	30	9.6	209	18	AAW14192 Mature pokeweed an
17	30	9.6	210	18	AAW14191 Mature pokeweed an
18	30	9.6	211	18	AAW14190 Mature pokeweed an
19	30	9.6	212	18	AAW14189 Mature pokeweed an
20	30	9.6	213	18	AAW14188 Mature pokeweed an
21	30	9.6	214	18	AAW14187 Mature pokeweed an
22	30	9.6	215	18	AAW14186 Mature pokeweed an
23	30	9.6	216	18	AAW14185 Mature pokeweed an
24	30	9.6	217	18	AAW14184 Mature pokeweed an
25	30	9.6	218	18	AAW14183 Mature pokeweed an
26	30	9.6	219	18	AAW14182 Mature pokeweed an
27	30	9.6	220	18	AAW14181 Mature pokeweed an
28	30	9.6	221	18	AAW14180 Mature pokeweed an
29	30	9.6	222	18	AAW14179 Mature pokeweed an
30	30	9.6	223	18	AAW14178 Mature pokeweed an
31	30	9.6	224	18	AAW14177 Mature pokeweed an
32	30	9.6	225	18	AAW14176 Mature pokeweed an
33	30	9.6	226	18	AAW14175 Mature pokeweed an
34	30	9.6	227	18	AAW14174 Mature pokeweed an
35	30	9.6	228	18	AAW14173 Mature pokeweed an
36	30	9.6	229	18	AAW14172 Mature pokeweed an
37	30	9.6	230	18	AAW14171 Mature pokeweed an
38	30	9.6	231	18	AAW14170 Mature pokeweed an
39	30	9.6	232	18	AAW14169 Mature pokeweed an
40	30	9.6	233	18	AAW14168 Mature pokeweed an
41	30	9.6	234	18	AAW14167 Mature pokeweed an
42	30	9.6	235	18	AAW14166 Mature pokeweed an
43	30	9.6	236	18	AAW14165 Mature pokeweed an
44	30	9.6	237	18	AAW14164 Mature pokeweed an
45	30	9.6	238	18	AAW14163 Mature pokeweed an

ALIGNMENTS

RESULT 1
AA837345
ID AA837345 standard; Protein: 294 AA.
XX AC AA837345;
XX DT 09-NOV-1993 (first entry)
XX DE Pokeweed antiviral protein.
XX KW Pokeweed: ricin; protein synthesis inhibitor; cancer;
XX KW polymerase chain reaction; PCR.
XX OS Phytolacca americana.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein /label= sig_peptide
XX FT /label= mat_protein
XX PN JP05137580-A.
XX PD 01-JUN-1993.
XX PF 20-NOV-1991; 91JP-0325672.
XX PR 20-NOV-1991; 91JP-0325672.
XX PA (NIDB) JAPAN TOBACCO INC.
XX DR WPI: 1593-211306/26.
XX DR N-PSDB: AAQ43967.

OY 1 MKVMLVVVVTLIAWLIAPSTCAINTITDAGNATINKYATFMSLRNOAKDPKLCY 60
DB 1 MKVMLVVVVTLIAWLIAPSTCAINTITDAGNATINKYATFMSLRNOAKDPKLCY 60
OY 61 IMLPDTNSTPKYLLVLOGANKLTITMLRRNNLYVMGYSDPFNGNCKRYHIFNDITST 120
DB 61 IMLPDTNSTPKYLLVLOGANKLTITMLRRNNLYVMGYSDPFNGNCKRYHIFNDITST 120
OY 121 ERTDVENTLSSSSSRVMSINYSLYPTMEKKAENSRNOVOLGIGILSSDICKISGVD 180
DB 121 ERTDVENTLSSSSSRVMSINYSLYPTMEKKAENSRNOVOLGIGILSSDICKISGVD 180
OY 181 SPVPKTEAFELLVAIQWSEAAARFYIENQVKTNFNRAFYDPKVINLEEKWKISIAH 240
DB 181 SPVPKTEAFELLVAIQWSEAAARFYIENQVKTNFNRAFYDPKVINLEEKWKISIAH 240
OY 241 NAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTQYONAMFQVISTY 300
DB 241 NAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTQYONAMFQVISTY 300
OY 301 YNYMSNLGDLFEFG 314
DB 301 YNYMSNLGDLFEFG 314

RESULT 2

ID Q8S946 PRELIMINARY: PRT: 262 AA.
AC Q8S946:
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE PAP-S2 (fragment).
CN PAPS2.
OS *Phytolacca americana* (Common pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_Taxid=3527;
RN [1]
KP SEQUENCE FROM N.A.
RA Honjo E., Watanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB071855; BAB86350.1;
FT NON_TER 1 1
FT NON_TER 262 262
SQ SEQUENCE 262 AA; 29486 MW; AF2D010A73C9D18B CRC64;

Query Match 82.4%; Score 1332; DB 10; Length 262;
Best Local Similarity 98.1%; Pred. No. 2.4e-96;
Matches 257; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 25 INTITDAGNATINKYATFMSLRNOAKDPKLCYGIPLPOTNSTPKYLLVLOGANKL 84
DB 1 INTITDAGNATINKYATFMSLRNOAKDPKLCYGIPLPOTNSTPKYLLVLOGANKL 60
OY 85 TITLMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLSSSSSRVMSINYN 144
DB 61 TITLMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLSSSSSRVMSINYN 120
OY 145 SLIYPTMEKKAENSRNOVOLGIGILSSDICKISGVDSPVPKTEAFELLVAIQWSEAAARF 204
DB 121 SLIYPTMEKKAENSRNOVOLGIGILSSDICKISGVDSPVPKTEAFELLVAIQWSEAAARF 180
OY 205 KYIENQVKTNFNRAFYDPKVINLEEKWKISIAHNAKNGALPKPLELVDAKGTWIVL 264
DB 181 KYIENQVKTNFNRAFYDPKVINLEEKWKISIAHNAKNGALPKPLELVDAKGTWIVL 240
OY 265 RVDEINRDVALLKYVNGTCOTT 286

DB 241 RVDEINRDVALLKYVNGTCOTT 262

RESULT 3

ID Q941G8 PRELIMINARY: PRT: 313 AA.
AC Q941G8:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN PAP.
OS *Phytolacca acinosa*.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_Taxid=107615;
RN [1]
RP SEQUENCE FROM N.A.
RA Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL; AY045785; AAL15442.1;
DR InterPro: IPR001574; RfP.
DR Pfam: PF00161; RfP; 1.
KW Hydrolase; Toxin.
SQ SEQUENCE 313 AA; 35059 MW; E478ED571C17885 CRC64;

Query Match 76.2%; Score 1231.5; DB 10; Length 313;
Best Local Similarity 75.9%; Pred. No. 2.2e-88;
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;

OY 1 MKVMLVVVVTLIAWLIAPSTCAINTITDAGNATINKYATFMSLRNOAKDPKLCY 60
DB 1 MKSMC--VVTISVWCLAPSTWAVNTIYNGVSTTISKYATFLDLNRNEAKDPSLKCY 58
OY 61 IMLPDTNSTPKYLLVLOGANKLTITMLRRNNLYVMGYSDPFNGNCKRYHIFNDITST 120
DB 59 IMLPDTNSTPKYLLVLOGANKLTITMLRRNNLYVMGYSDPFNGNCKRYHIFNDITST 178
OY 121 ERTDVENTLSSSSSRVMSINYSLYPTMEKKAENSRNOVOLGIGILSSDICKISGVD 180
DB 119 ERQDVTETLCPNPSRVSKNINYSRYPTLESKAGVSKSVOVLGIGILSDNICKISGV 178
OY 181 SPVPKTEAFELLVAIQWSEAAARFYIENQVKTNFNRAFYDPKVINLEEKWKISIAH 240
DB 179 SFTEKTEAFELLVAIQWSEAAARFYIENQVKTNFNRAFYDPKVINLEEKWKISIAH 238
OY 241 NAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTQYONAMFQVISTY 299
DB 239 DAKNGVLPKPLELVDAKGTWIVLRVDDIKPUVALCUNYVGSCOTTQYONAMFPOLIMST 298
OY 300 YNYMSNLGDLFEFG 314
DB 299 YNYMANLGDLPFG 313

RESULT 4

ID Q9XFF8 PRELIMINARY: PRT: 315 AA.
AC Q9XFF8:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN PIP2.
OS *Phytolacca insularis*.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 28, 2003, 09:51:54 ; Search time 87 Seconds
(without alignments)
743.664 Million cell updates/sec

US-09-978-274A-2

Perfect score: 1617

Sequence: 1 MKVMLVVVTLIAWLIAPT.....VIITSYVYVMSNLGLFEGF 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPREMBL_21.*
- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1617	100.0	314	10	P93444	Phytolacca
2	1332	82.4	262	10	O8S946	Phytolacca
3	1231.5	76.2	313	10	O941C8	Phytolacca
4	1147.5	71.0	315	10	O9XFF8	Phytolacca
5	1127	69.7	339	10	O8RIA4	Phytolacca
6	1099.5	68.0	261	10	O8S947	Phytolacca
7	953	58.9	237	10	O9ATB3	Phytolacca
8	702	43.4	302	10	P93077	Clerodendru
9	455.5	28.2	289	10	P93261	mesembryant
10	406	25.1	272	10	O39418	beta vulgar
11	393	24.9	279	10	O9M5K6	Chenopodium
12	363.5	22.5	294	10	O9AUE3	Chenopodium
13	363.5	22.5	294	10	O93Y65	dianthus ch
14	357.5	22.1	294	10	O93Y64	dianthus ch
15	349.5	21.6	294	10	O93Y66	dianthus ch
16	321.5	19.9	258	10	O9S9E4	gelonium mu

Qy 145 SLYPTMEKKAENVSRNOVQLGTOILSSDTGKISGVDSFPVKTEAFLLVATQMVSEAAARF 204
Db 120 GLYPTLEKKAGVTSRNEVQLGTOILSSDKIGKISGOGSFTKIERDFLLVATQMVSEAAARF 179
Qy 205 KYIENOVKTNENRATYPPDKVINLEEKWKCTSEATHNAKNGALPKPLELVDAKGTWKIVL 264
Db 180 KYIENOVKTNENRDFSPNDKVLDELLENKGTSTATHNSKNGALPKPLELKNADGTWKIVL 239
Qy 265 RVDEINROVALLKYVNGTCQTT 286
Db 240 RVDEIKPOVGLLNYNGTCQAT 261

Search completed: May 28, 2003, 09:56:05
Job time : 78 secs

09978274

SRN

Printed 11/17/2004

06/02/2003

Db 240 RVDEIKPDVGLLYVNGTQCOAT 261

RESULT 14
AAW21708
ID AAW21708 standard: Protein; 261 AA.
XX
AC AAW21708;
DT 26-SEP-1997 (first entry)
XX
DE PAP-S RIP.
XX
KW pro-Ribosome Inactivating Protein; prORIP; peptide linker; cancer;
KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
XX
OS *Phytolacca americana*.
XX
FH Key
FT Region
FT /note= "position of possible insertion of internal
peptide linker sequence"
XX
XX US5635384-A.
XX
XX 03-JUN-1997.
XX
XX 11-JUN-1990; 90US-0535636.
XX
XX 09-DEC-1992; 92US-0987927.
XX 11-JUN-1990; 90US-0535636.
XX 26-JAN-1995; 95US-0378761.
XX
XX (DOWC) DOWELANCO.
XX
XX Hey TD, Morgan ABR, Walsh TA;
XX
XX WPI: 1997-309831/28.
XX
XX Inactive precursor of maize ribosome-inactivating protein - also
XX chimeric ribosome-inactivating protein precursors containing
XX internal linker sequences
XX
XX Claim 2: Column 125-126; 121pp; English.
XX
XX The sequences given in AAW21698-710 represent Ribosome Inactivating
XX Proteins (RIP's), which may be used in the construction of the
XX proRIP of the invention. The proRIP has a selectively removable,
XX internal peptide linker. The precursor sequence is incapable of
XX inactivating eukaryotic ribosomes, but can be converted by removal
XX of the linker into a protein having alpha and beta fragments and being
XX capable of inactivating eukaryotic ribosomes. RIPs are potent
XX inhibitors of eukaryotic protein synthesis. They possess a highly
XX specific N-glycosidase activity which cleaves the glycosidic bond of
XX adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
XX cellular proliferation of cells, e.g. cancer cells and HIV-infected T
XX cells. The inactive proRIP proteins make it possible to provide protein
XX synthesis inhibitors with uses in practical and improved ways not before
XX possible. The RIP can be used to make cytotoxic conjugates.
XX
XX Sequence 261 AA;
SQ

Query Match 67.8%; Score 1096.5; DB 18; Length 261;
Best Local Similarity 82.8%; Pred. No. 31e-98;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
Qy 25 INITITDAGNATINKYATFMESLRNKAOKPKLKCVCYGPMLPDTNSTPKYLLVVKLOCANLK 84
Db 1 INITITDAGNATINKYATFMESLRNKAOKPKLKCVCYGPMLPDTNSTPKYLLVVKLOCANLK 60
Qy 85 TITLMLRRNLVYMGYSDDPYD-NKCRHYHFNIDIKGTEYSDVENTICLSSSSSRVAMSNYN 144

Db 61 TITLMLRRNLVYMGYSDDPYD-NKCRHYHFNIDIKGTEYSDVENTICLSSSSSRVAMSNYN 119
Qy 145 SLYPTMEKKAENSRNQVGLGTOILSSDQKISGVDSFPVKTEAPFLLVAIONVSAAR 204
Db 120 GLYPTLEKKACVTSRNEVOLGQIISDDICKISGVDSFTEKTEAKFELVAIONVSAAR 179
Qy 205 KYIENOVKTNFRAFYPPKPVINLEEKWKQISEATHNAKNGALPKPLVLDAGKATL 264
Db 180 KYIENOVKTNFRDFSPNDKVLDEENWCKJSTAIHNSKNGALPKPLVLDAGKATL 219
Qy 265 RVDEIKPDVGLLYVNGTQCOAT 286
Db 240 RVDEIKPDVGLLYVNGTQCOAT 261

RESULT 35
AAR37298
ID AAR37298 standard: protein; 261 AA.
XX
AC AAR37298;
DT 13-SEP-1993 (first entry)
XX
XX Plant type I RIP pokeweed antiviral protein.
XX
XX Type I ribosome-inactivating protein; ricin; gelonin; momordin;
XX immunoconjugate; autoimmune disease; cell killing; toxin; PAP.
XX
XX WC9309130-A.
XX
XX 13-MAY-1993.
XX
XX 04-NOV-1992; 92WQ-US09487.
XX
XX 04-NOV-1991; 91US-0787567.
XX 19-JUN-1992; 92US-0901707.
XX
XX (XOMA) XOMA CORP.
XX
XX Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX WPI: 1993-167617/20.
XX
XX Analogues of type I ribosome inactivating protein - useful as
XX cytotoxic agents, immuno toxins for treating autoimmune diseases,
XX cancer, graft versus host disease and selective cell killing in vivo
XX
XX Disclosure: Page 99-100; 163pp; English.
XX
XX The invention covers analogues of Type I RIPs. Pokeweed antiviral
XX protein is a Type I RIP and the analogues of the invention have a
XX Cys available for intermolecular disulphide bonding at an amino acid
XX position corresp. to a position not naturally available for bonding;
XX the Cys residue is located in the C-terminal region of the analogue
XX between a position corresp. to amino acid 251 and the C-terminus of
XX ricin A chain. The analogues are pref. joined via a disulphide
XX linkage to a molecule which specifically binds to a target cell, e.g.
XX an antibody fragment.
XX
XX Sequence 261 AA;
SQ

Query Match 67.4%; Score 1089.5; DB 14; Length 261;
Best Local Similarity 82.4%; Pred. No. 1.5e-97;
Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;
Qy 25 INITITDAGNATINKYATFMESLRNKAOKPKLKCVCYGPMLPDTNSTPKYLLVVKLOCANLK 84
Db 1 INITITDAGNATINKYATFMESLRNKAOKPKLKCVCYGPMLPDTNSTPKYLLVVKLOCANLK 60
Qy 85 TITLMLRRNLVYMGYSDDPYD-NKCRHYHFNIDIKGTEYSDVENTICLSSSSSRVAMSNYN 144
Db 61 TITLMLRRNLVYMGYSDDPYD-NKCRHYHFNIDIKGTEYSDVENTICLSSSSSRVAMSNYN 119

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XX NB: A protein comprising 261 amino acids is claimed.
CC PAP has a similar activity to ricin, i.e. inhibits protein synthesis.
CC The protein may be obtained all year round by recombinant DNA
CC techniques. PAP can be used partic. against cancer and as an
CC agricultural chemical.
CC Total mRNA, is extracted from the seeds, leaves and roots of
CC pokeweed and used to prepare cDNA using PCR. The resultant cDNA is
CC used to prepare two DNA fractions, which are introduced into a
CC cloning vector EMBL3 and then into host E.coli PLK-17 (P2) to
CC produce PAP.
XX Sequence 294 AA:

Query Match 68.9%; Score 1113.5; DB 14; Length 294;
Best Local Similarity 75.4%; Pred. No. 8.3e-100;
Matches 221; Conservative 27; Mismatches 42; Indels 3; Gaps 3;
Qy 1 MKMVLVVVTLIAHLIAAPTSTCAINTITFDAGNATINKYATFMESLRNQAKDKPKLCYCG 60
Db 1 MKMVLVVVWMLSLILKPPSTWAINITFDVGNATINKYATFMESLRNQAKDKPKLCYCG 60
Qy 61 IPMLPDTNSTPKYLLVLOGANLKTITLMLRRNLYVMGYSDPENGKCRVHIENDIT-S 119
Db 61 IPMLPDTNSTPKYLLVLOGANLKTITLMLRRNLYVMGYSDPENGKCRVHIENDIT-S 119
Qy 120 TERTDVENTLCSSSSRVMSINSLYPTMEKKAENSRNOVOLGIOLSSDICKISGV 179
Db 120 TERTDVENTLCSSSSRVMSINSLYPTMEKKAENSRNOVOLGIOLSSDICKISGV 179
Qy 180 DSPVPKTEAFELLVAIONVSEAAKPKYIENOVKTNFRAFPDPKVINLEEKWKISAI 239
Db 180 DSPVPKTEAFELLVAIONVSEAAKPKYIENOVKTNFRAFPDPKVINLEEKWKISAI 239
Qy 240 HNANGALPKLELVDAKGTWKIVLRVDEINRDVALLKYVNGTCOTTYYONAMF 292
Db 240 HNANGALPKLELVDAKGTWKIVLRVDEINRDVALLKYVNGTCOTTYYONAMF 292

RESULT 11
AAR13112
ID AAR13112 standard; protein: 261 AA.
AC AAR13112;
XX 08-OCT-1991 (first entry)
XX Anti-viral protein.
XX Protein synthesis inhibitor; plant virus.
XX Phytoacca americana.
XX Key Location/Qualifiers
XX Disulfide-bond 84...105
XX Disulfide-bond 34...258
XX JP03145498-A.
XX 20-JUN-1991.
XX 27-OCT-1989; 89JP-0281373.
XX 27-OCT-1989; 89JP-0281373.
XX (SUMO) SUMITOMO CHEM IND KK.
XX WPI; 1991-226467/31.
XX Bioactive protein of phytoacca amepicana - used as protein
XX synthesis inhibitor against infection caused by plant virus.
XX Claim 1: Fig 1: 6 pp: Japanese.

06/02/2003

XX The sequence codes for a bioactive protein which can be used to
CC inhibit infection by plant viruses. It is obtd. from the plant
CC seeds but high yields and purity can be obtd. by synthesising the
CC gene encoding it and introducing it into E.coli, yeast, or animal
CC or plant cells.
XX Sequence 261 AA:
Query Match 67.8%; Score 1056.5; DB 12; Length 261;
Best Local Similarity 82.8%; Pred. No. 3.1e-98;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

Qy 25 INTITFDAGNATINKYATFMESLRNQAKDKPKLCYCGIPMLPDTNSTPKYLLVLOGANLK 84
Db 1 INTITFDAGNATINKYATFMESLRNQAKDKPKLCYCGIPMLPDTNSTPKYLLVLOGANLK 84
Qy 85 TITLMLRRNLYVMGYSDPENGKCRVHIENDITSTERTDVENTLCSSSSRVMSINYN 144
Db 61 TITLMLRRNLYVMGYSDPYD-NKCRVHIENDIKCTEYSDVENTLCPSSAPRVAKIPINYN 119
Qy 145 SLYPTMEKKAENSRNOVOLGIOLSSDICKISGVSDPENGKCRVHIENDITSTERTDVENTLCSSSSRVMSINYN 204
Db 120 GLYPTLEKKAQVTSRNEVOLGIOLSSDICKISGVSDPENGKCRVHIENDITSTERTDVENTLCSSSSRVMSINYN 179
Qy 205 KYIENOVKTNFRAFPDPKVINLEEKWKISAIHNAKNGALPKLELVDAKGTWKIVL 264
Db 180 KYIENOVKTNFRAFPDPKVINLEEKWKISAIHNAKNGALPKLELVDAKGTWKIVL 239
Qy 265 RVDEINRDVALLKYVNGTCOTT 286
Db 240 RVDEINRDVALLKYVNGTCOTT 261

RESULT 12
AAR74184
ID AAR74184 standard; protein: 261 AA.
AC AAR74184;
XX 01-JAN-1996 (first entry)
XX Type I RIP pokeweed anti-viral protein (PAP) isolated from seeds.
XX Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin.
XX Pokeweed.

XX Key Location/Qualifiers
XX Misc-difference 16 /label= invariant residue
XX Misc-difference 24 /note= "in ricin A-chain and the Type I RIPS"
XX Misc-difference 24 /label= see above
XX Misc-difference 72 /label= see above
XX Misc-difference 122 /label= see above
XX Misc-difference 144 /label= see above
XX Misc-difference 175...176 /label= see above
XX Misc-difference 178 /label= see above
XX Misc-difference 207 /label= see above
XX US5416202-A.
XX 16-MAY-1995.
XX 09-DEC-1992; 92US-0988430.
XX

SRNT

Printed 11/17/2004

Query Match 71.0%; Score 1147.5; DB 19; Length 315;
Best local Similarity 72.2%; Pred. No. 4.5e-103;
Matches 229; Conservative 36; Mismatches 47; Indels 5; Gaps 4;

QY 1 MKVNLVVVVTLIAWLIAPSTGCAI--NTITFDAGNATINKYATFMESLRNOAKDKLKC 58
DB 1 MKMNVLVMTITAWLIAPASTWAASNPITFEVGNATINKYATFMESLRNOAKDPNLQC 60
QY 59 YGIMPLDPTNSTPKYLLVKLGANLKTITMLRRNNLYVMGYSDPPFNGNKCRIYHFNIDIT 118
DB 61 YGIMPLDPTNSTPKYLLVKLGANLKTITMLRRNNLYVMGYADTYN-NKCRYHIFKDIS-119
QY 119 -STERTDVENTLCSSSSRVAMSINYSLYPTMEKKAEVNSRNOVQIGIQLSSDICKIS 177
DB 120 NTTERNOVMTLCPNMSRVKNTSYDSSYPALCKKVG-RSRKVKVQIGIQLNSDIKIY 178
QY 178 GVDSPFVKTEAFFLLVAIQMVSEAAKPKYIENOVKTNFRAFYDPKPVJNLEEKWKIKR 237
DB 179 GVDVNEKTEAEFLLVAIQMVPEATREKYIENOVKTNFRAFYDNKVLNLEETWGLIST 238
QY 238 AIHNAKNGALPKLELDVDAKTKWIVLVRVDEIKPDVGLLVYVDGTCOTTYQSDMFQRI 297
DB 239 AIHDAKNGALT KPLELINEDGTKWIVLVRVDEIKPDVGLLVYVDGTCOTTYQSDMFQRI 298
QY 298 STYYNYMNSLGDLEFGF 314
DB 299 STYYNYIVNLGDQFEFG 315

RESULT 9
AAM53033
ID AAM53033 standard; Protein: 315 AA.
XX AC AAM53033;
XX DT 19-MAR-2002 (first entry)
XX DE Phytolacca insularis antiviral protein (PIP).
XX KW Antiviral protein; PIP; cloning vector.
XX OS Phytolacca insularis.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein /label= Signal_peptide 25..315
XX FT Protein /label= Mature_PIP 196..208
XX FT Region /note= "This region is highlighted in the specification, indicating that it has some significance"
XX KR98021298-A.
XX PD 25-JUN-1998.
XX PF 16-SEP-1996; 96KR-0040110.
XX PR 16-SEP-1996; 96KR-0040110.
XX PA (JINR-) JIN RO LTD.
XX PI Moon YH, Choi JN, Yoon YC, Jin JH, Hong EJ, Lee JH, Chang JI;
XX PI Park YC, Choi GH, Kim CH, Kim MG, Song SG, Lee JS, Choi YD;
XX DR WPI: 1999-299928/25.
XX DR N-PSDB: ABA96543.
XX XX Cloning vector using gene of Phytolacca insularis antiviral protein (PIP) -
XX PS Claim 1: Fig 1; 9pp; Korean.

CC The invention relates to cloning vectors comprising a gene encoding
CC the Phytolacca insularis antiviral protein, PIP (ABA96543, AAM53033), or
CC a fragment thereof. The present sequence represents PIP.
XX SQ Sequence 315 AA:
Query Match 71.0%; Score 1147.5; DB 20; Length 315;
Best local Similarity 72.2%; Pred. No. 4.5e-103;
Matches 229; Conservative 36; Mismatches 47; Indels 5; Gaps 4;

QY 1 MKVNLVVVVTLIAWLIAPSTGCAI--NTITFDAGNATINKYATFMESLRNOAKDKLKC 58
DB 1 MKMNVLVMTITAWLIAPASTWAASNPITFEVGNATINKYATFMESLRNOAKDPNLQC 60
QY 59 YGIMPLDPTNSTPKYLLVKLGANLKTITMLRRNNLYVMGYSDPPFNGNKCRIYHFNIDIT 118
DB 61 YGIMPLDPTNSTPKYLLVKLGANLKTITMLRRNNLYVMGYADTYN-NKCRYHIFKDIS 119
QY 119 -STERTDVENTLCSSSSRVAMSINYSLYPTMEKKAEVNSRNOVQIGIQLSSDICKIS 177
DB 120 NTTERNOVMTLCPNMSRVKNTSYDSSYPALCKKVG-RSRKVKVQIGIQLNSDIKIY 178
QY 178 GVDSPFVKTEAFFLLVAIQMVSEAAKPKYIENOVKTNFRAFYDPKPVJNLEEKWKIKR 237
DB 179 GVDVNEKTEAEFLLVAIQMVPEATREKYIENOVKTNFRAFYDNKVLNLEETWGLIST 238
QY 238 AIHNAKNGALPKLELDVDAKTKWIVLVRVDEIKPDVGLLVYVDGTCOTTYQSDMFQRI 297
DB 239 AIHDAKNGALT KPLELINEDGTKWIVLVRVDEIKPDVGLLVYVDGTCOTTYQSDMFQRI 298
QY 298 STYYNYMNSLGDLEFGF 314
DB 299 STYYNYIVNLGDQFEFG 315

RESULT 10
AAR37345
ID AAR37345 standard; Protein: 294 AA.
XX AC AAR37345;
XX DT 09-NOV-1993 (first entry)
XX DE Pokeweed antiviral protein.
XX KW Pokeweed; ricin; protein synthesis inhibitor; cancer;
XX KW polymerase chain reaction: PCR.
XX OS Phytolacca americana.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein /label= sig_peptide 25..294
XX FT Protein /label= mat_protein
XX JPO5137580-A.
XX PD 01-JUN-1993.
XX PF 20-NOV-1991; 91JP-0329672.
XX PR 20-NOV-1991; 91JP-0329672.
XX PA (NISR) JAPAN TOBACCO INC.
XX DR WPI: 1993-211306/26.
XX DR N-PSDB: AAO43967.
XX XX New pokeweed antiviral protein (PAP) with similar activity to
XX XX ricin - used to treat cancer and as an agricultural chemical
XX PS Claim 1: Page 11-13; 14pp; Japanese.

AAW26773	standard; Protein; 292 AA.
AAW26773	
08-JUN-1998	(first entry)
Phytolacca insularis	antiviral protein gPIP2.
Antiviral protein: gPIP2;	virucide; transgenic plant;
virus resistance; immunoconjugate;	AIDS; cancer; therapy.
Phytolacca insularis Nakai.	
Key	Location/Qualifiers
Active-site	172..184
Misc-difference	239
/note=	"encoded by ATG"
FP808902-A2.	
26-NOV-1997.	
30-SEP-1996;	96EP-0307159.
22-MAY-1996;	96KR-0017404.
(JINR-) JIN RO LTD.	
Choi J, Choi K, Choi Y, Hong E, Jin J, Kim C;	
Kim M, Lee J, Lee J, Moon Y, Song S, Yun Y.	
WPI; 1998-001788/01.	
N-PSDB: AAT99556.	
Antiviral proteins of Phytolacca insularis Nakai and their genes	
used in plant antiviral agents and immunoconjugates for the	
treatment of AIDS and cancer	
Claim 7; Page 10-12; 26pp; English.	
This polypeptide comprises a mature novel antiviral protein,	
designated gPIP2, of Phytolacca insularis Nakai. Its amino	
acid sequence was deduced from the gPIP2 gene (see AAT99556) that	
was isolated from leaf genomic DNA. The sequence shows 93.1%	
homology to the known antiviral protein cPAP and 82.5% homology to	
the known antiviral protein cPIP. Another novel antiviral	
protein, gPIP50 (see AAW26774), from P. insularis Nakai has also been	
identified. A claimed process for producing recombinant gPIP2	
involves culturing E. coli XL1-Blue MRF' gPIP2 (KCCM-10080),	
inducing expression of the protein using IPTG, harvesting the	
inclusion bodies and purifying the recombinant protein. gPIP2	
antiviral protein inhibits protein synthesis. It can be expressed	
in transgenic plants to provide viral resistance and can be used as	
an active ingredient of plant antiviral agents. It can also be	
employed in the manufacture of immunoconjugates for the treatment	
of AIDS and cancer.	
Sequence 292 AA;	
Query Match	71.8%; Score 1160.5; DB 19; Length 292;
Best Local Similarity	76.3%; Pred. No. 2.2e-104;
Matches	222; Conservative 30; Mismatches 38; Indels 1; Gaps
25 INITITDAGNATINKYATFMESLRNQAOKPKLKCYGIPMLPDTNTPKYLVLKQGANLK 84	
2 VNTIIYVGGTTISKYATFDLNRNKAEDSLKCYGIPMLPTNPKNPKYLVKLGQSNK 61	
85 TTILMLPRNNLYVMGYSDFPNGNKRVHFNIDTSTERTDVENTLCSSSSSRVMSINYN 141	
62 TTILMLRNNLYVMGYSDFPNGNKRVHFNIDTSTERTDVENTLCSSSSSRVMSINYN 121	
145 SLYPTMKEKKAEVNRRNOVLGIIQLSSLDIGKISGVDSFPYVKTEAFLLVAIQWSEAFR 204	

DB	122	SRYPTLESKACVYKRSQVGLG101JLJSDICK1SCVTSFTFEKYPAEFLVAIOWVSFAHF	18
QY	205	KYIENQVKTNFNRAFYDPKVINLEEKWKGISAIHNAKNGALPKPLELVDAGTKWIVL	264
DB	182	KYIENQVKTNFNRAFPNPKVLNLEETGCK1STALHDAKNGVLPKPLELVDASGANNIVL	241
QY	265	KVDEINRDVALLKYVNGTCUTTY-QNAMI:SQVLIISYYMYMSNLGDLPECF	314
DB	242	RVDGIDKPDVALLNYVSGSCOTNYNQAMPJLIMSTYYNYMHAGDQFEGF	292
RESULT 8			
AAW26774	AAW26774 standard; Protein; 315 AA.		
ID	AAW26774:	(first entry)	
XX	08-JUN-1998		
XX	Phytolacca insularis antiviral protein gPIP50.		
XX	Antiviral protein: gPIP50; virucide; transgenic plant;		
KW	virus resistance; immunoconjugate; AIDS; cancer; therapy.		
KX	Phytolacca insularis Nakai.		
OS			
XX	Key	Location/Qualifiers	
FH	Peptide	1..24	
FT		/label= Sig_peptide	
FT	Active-site	196..208	
FT		/note= "putative active site"	
XX	EP808902-A2.		
PN	26-NOV-1997.	96EP-0307159.	
XX	30-SEP-1996;	96EP-0307159.	
PF	22-MAY-1996;	96RR-0017404.	
XX	(JINR-) JIN RO LTD.		
PI	Choi J, Choi Y, Hong E, Jin J, Kim C;		
PI	Kim M, Lee J, Lee J, Moon Y, Song S, Yun Y;		
XX	WPI: 1998-001784/01.		
DR	N-PSDB: AAT99557.		
XX	Antiviral proteins of Phytolacca insularis Nakai and their genes		
PT	useful in plant antiviral agents and immunoconjugates for the		
PT	treatment of AIDS and cancer		
XX	Claim 7: Fig 5: 26pp; English.		
XX	This polypeptide comprises a mature novel antiviral protein,		
CC	designated gPIP50, of Phytolacca insularis Nakai. Its amino		
CC	acid sequence was deduced from the gPIP50 gene (see AAT99557)		
CC	that was isolated from leaf genomic DNA. The sequence shows 64.4%		
CC	homology to the known antiviral protein cPIP and 84% homology to		
CC	the known antiviral protein alpha-PAP. Another novel antiviral		
CC	protein, gPIP2 (see AAW26773), from P. insularis Nakai has also been		
CC	identified. A claimed process for producing recombinant gPIP50		
CC	involves cultivating E. coli XL1-Blue MRF' gPIP50 (KCCM-10081),		
CC	inducing expression of the protein using IPTG, harvesting the		
CC	inclusion bodies and purifying the recombinant protein. gPIP50		
CC	antiviral protein inhibits protein synthesis. It can be expressed		
CC	in transgenic plants to provide viral resistance and can be used as		
CC	an active ingredient of plant antiviral agents. It can also be		
CC	employed in the manufacture of immunoconjugates for the treatment		
CC	of AIDS and cancer.		
XX	Sequence	315 AA;	

315 AA;

OS XX

DT 22-FEB-1995 (first entry)
XX Pokeweed Antiviral Protein mutant PAP-9.
DE
XX
XX Pokeweed antiviral protein; PAP; ribosome inactivating protein;
KW RIP type I; immunotoxin; cell targeting; mutant.
XX
XX Phytolacca americana.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 196
FT /note- "wild-type Phe is replaced by Tyr"
FT Misc-difference 211
FT /note- "wild-type Lys is replaced by Arg"
XX
XX PR2699553-A.
XX
XX 24-JUN-1994.
PD
XX
XX 09-DEC-1992: 92PR-0014821.
PF
XX
XX 09-DEC-1992: 92PR-0014821.
PK
XX
XX (INNO-) INNOTHERAPIE LAB.
PA
XX
XX Dore J, Gras E, Wijdenes J.
PI
XX
XX WPI: 1994-227165/28.
DR
XX
XX Gene encoding mutant protein toxic to eukaryotic but not
PT prokaryotic cells esp. mutant pokeweed antiviral protein - are
PT useful in immunotoxin prodn., protection against viral infection
PT and for targeted cell destruction
XX
XX Claim 10; Fig 1; 25pp; French.
PS
XX
XX Mutants of type I Ribosome Inactivating Proteins which are toxic to
CC eukaryotic, but not prokaryotic, cells are preferably derived from
CC the wild-type Pokeweed Antiviral Protein (PAP) (AAR57153).
CC Specifically, the mutants are PAP1 (with Gly replacing wild-type
CC Arg at position 68) and PAP9 (with Tyr replacing wild-type Phe and
CC Arg replacing wild-type Lys at positions 196 and 211, respectively).
XX
XX Sequence 292 AA;

Query Match 72.0%; Score 1164.5; DB 15; Length 292;
Best Local Similarity 76.3%; Pred. No. 8.9e-105;
Matches 222; Conservative 32; Mismatches 36; Indels 1; Gaps 1:
QY 25 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLPDTNSTPKYLLVKGANLK 84
DB 2 VNTIYVNGSTTSKYATFLDLRNEAKDPSLCYGIPLPNTNTNPKYVLVQLGSKNK 61
QY 85 TITLMLRRNNLYVMGYSDFPENGKCRVHIFNDITSTERTDVENTLCSSSSRVAMSYN 144
DB 62 TITLMLRRNNLYVMGYSDFPENGKCRVHIFNDISGTERQDVETTLCPNANSRVSKNIFD 121
QY 145 SLYPTMEKKAENSRNOVQLGIQLSSDIGKISGVDSFPVKTEAFFLLVAIQMYSAAKF 204
DB 122 SRYPTLESKAGVKSRSOVQLGIQLDSNIGKISGVMSFTEKTEAEFLVAIQMYSAAKF 181
QY 205 KYIENQVKTNFNRAFYPPKPVNLEEKWKISSEATHNAKNGALPKPLELVDAKGTWIVL 264
DB 182 KYIENQVKTNFNRAFNPNKPVNLEQETWGRISTALHDAKNGVLPKPLELVDAKGTWIVL 241
QY 265 RVDEINRDVALLKYVNGTCQTTY-QNAMFSQVITSTYNYMNSLGLDFEGF 314
DB 242 RVDEIKPDVALLNYVGGSCQTTYNQNAMEPQLIMSTYNYMNSLGLDFEGF 292

RESULT 6
AAR57153
ID AAR57153 standard; protein; 292 AA.

XX AAR57153;
XX 22-FEB-1995 (first entry)
XX Pokeweed Antiviral Protein mutant PAP-1.
DE
XX
XX Pokeweed antiviral protein; PAP; ribosome inactivating protein;
KW RIP type I; immunotoxin; cell targeting; mutant.
XX
XX Phytolacca americana.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 68
FT /note- "wild-type Arg is replaced by Gly"
XX
XX PR2699553-A.
XX
XX 24-JUN-1994.
PD
XX
XX 09-DEC-1992: 92PR-0014821.
PF
XX
XX 09-DEC-1992: 92PR-0014821.
PK
XX
XX (INNO-) INNOTHERAPIE LAB.
PA
XX
XX Dore J, Gras E, Wijdenes J.
PI
XX
XX WPI: 1994-227165/28.
DR
XX
XX Gene encoding mutant protein toxic to eukaryotic but not
PT prokaryotic cells esp. mutant pokeweed antiviral protein - are
PT useful in immunotoxin prodn., protection against viral infection
PT and for targeted cell destruction
XX
XX Claim 10; Fig 1; 25pp; French.
PS
XX
XX Mutants of type I Ribosome Inactivating Proteins which are toxic to
CC eukaryotic, but not prokaryotic, cells are preferably derived from
CC the wild-type Pokeweed Antiviral Protein (PAP) (AAR57153).
CC Specifically, the mutants are PAP1 (with Gly replacing wild-type
CC Arg at position 68) and PAP9 (with Tyr replacing wild-type Phe and
CC Arg replacing wild-type Lys at positions 196 and 211, respectively).
XX
XX Sequence 292 AA;

Query Match 72.0%; Score 1163.5; DB 15; Length 292;
Best Local Similarity 76.6%; Pred. No. 1.1e-104;
Matches 223; Conservative 30; Mismatches 37; Indels 1; Gaps 1:
QY 25 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLPDTNSTPKYLLVKGANLK 84
DB 2 VNTIYVNGSTTSKYATFLDLRNEAKDPSLCYGIPLPNTNTNPKYVLVQLGSKNK 61
QY 85 TITLMLRRNNLYVMGYSDFPENGKCRVHIFNDITSTERTDVENTLCSSSSRVAMSYN 144
DB 62 TITLMLRRNNLYVMGYSDFPENGKCRVHIFNDISGTERQDVETTLCPNANSRVSKNIFD 121
QY 145 SLYPTMEKKAENSRNOVQLGIQLSSDIGKISGVDSFPVKTEAFFLLVAIQMYSAAKF 204
DB 122 SRYPTLESKAGVKSRSOVQLGIQLDSNIGKISGVMSFTEKTEAEFLVAIQMYSAAKF 181
QY 205 KYIENQVKTNFNRAFYPPKPVNLEEKWKISSEATHNAKNGALPKPLELVDAKGTWIVL 264
DB 182 KYIENQVKTNFNRAFNPNKPVNLEQETWGRISTALHDAKNGVLPKPLELVDAKGTWIVL 241
QY 265 RVDEINRDVALLKYVNGTCQTTY-QNAMFSQVITSTYNYMNSLGLDFEGF 314
DB 242 RVDEIKPDVALLNYVGGSCQTTYNQNAMEPQLIMSTYNYMNSLGLDFEGF 292

RESULT 7
AAR57153

09978274

AC AAR48548;
XX 04-SEP-1994 (first entry)
XX Sequence of Phytolacca antiviral protein (PAP).
XX Antiviral protein; PAP; virus-resistance; transgenic plant.
XX Phytolacca americana L.
XX EP585554-A.
XX 09-MAR-1994.
XX 30-JUN-1993; 93EP-0110445.
XX 16-AUG-1992; 92KR-0014895.
XX (JINR-) JIN RO LTD.
XX (SHIN-) SHINRO KK.
XX Choi K, Jeon H, Jeong H, Kim M, Lee K, Moon Y;
XX Na B;
XX WPI: 1994-076002/10.
XX N-PSDB; AAQ56672.
XX Expression vector for phytolacca antiviral protein - used for
XX producing transgenic virus-resistant plants and for producing the
XX antiviral agent
XX Disclosure: Fig 1; 15pp; English.
XX To isolate PAP gene, total cellular mRNA was purified from leaves of
XX Phytolacca americana L. obtd. in Korea. A cDNA library was
XX constructed. The PAP gene was selected by immunoscreening employing
XX anti-PAP antibody. A deletion mutant was prepd. from the isolated
XX PAP gene, and the DNA sequence of the PAP genomewas determined.
XX
XX Sequence 313 AA:

Query Match 76.08; Score 1229.5; DB 15; Length 313;
Best Local Similarity 75.68; Pred. No. 4.6e-111;
Matches 238; Conservative 33; Mismatches 41; Indels 3; Gaps 2;
Qy 1 MKVLLVVVTIAMIAPTSTCAINTITFDAGNATINKYATFMESLRNQAKDKPKCYG 60
Db 1 MKSLVVTISI--WLLAPTSTWAVNTIYVVGSTTISKYATFLNDRNEAKDPSLKYG 58
Qy 61 IPMLPDTNSTPKYLLVKGANLKTITLMLRRNNLYVMGSDPPFNKCRHYHFNIDTST 120
Db 59 IPMLPNTNPKYLVVLOGSNKKTITLMLRRNNLYVMGSDPPFTTKCRHYHFNIDSGT 118
Qy 121 ERTDVENTLCSRSSRVAMSYNSLYPTMEKKAQVNSRNOVOLGQIOLSSDICKISQVD 180
Db 119 ERQDVTTLCPNANSRVSKNFDSRYPTLESKAGVRSQVQLGQIOLDSNIGKISGV 178
Qy 181 SFPVKTEAFFLVAIOMVSEARFYIENQVKTENRFAFYDPKVINLEEKWGIKISEAH 240
Db 179 SFTKTEAEFLVLAQVOMVSEARFYIENQVKTENRFAFNPNKVLNLQETWGIKISTAH 238
Qy 241 NAKNGALPKPLVDKAGTKWIVLRVDEINRDVALLKYVNGTCQTTY-ONAMFSQVILST 299
Db 239 DAKNGVLPKPLVDASGAKWIVLRVDEIKPDVALLNVVGGSCQTTYQNAMFPOLIMST 298
Qy 300 YNNYNSNLGDLFEFG 314
Db 299 YNNYNSNLGDLFEFG 313
RESULT 4
AAR57152
ID AAR57152 standard; protein: 292 AA.

XX AAR57152;
XX 22-FEB-1995 (first entry)
XX Wild-type pokeweed Antiviral Protein (PAP).
XX Pokeweed antiviral protein; PAP; ribosome inactivating protein;
XX RIP type I; Immunotoxin; cell targeting.
XX Phytolacca americana.
XX FR2699553-A.
XX 24-JUN-1994.
XX 09-DEC-1992; 92FR-0014021.
XX 09-DEC-1992; 92FR-0014821.
XX (INNO-) INNOTHERAPIE LAB.
XX Dore J, Gras E, Wijdenes J;
XX WPI: 1994-227165/28.
XX Gene encoding mutant protein toxic to eukaryotic but not
XX prokaryotic cells esp. mutant pokeweed antiviral protein - are
XX useful in immunotoxin prodn... protection against viral infection
XX and for targeted cell destruction
XX
XX Disclosure: Fig 1; 25pp; French.
XX Mutants of type I Ribosome Inactivating Proteins which are toxic to
XX eukaryotic, but not prokaryotic, cells are preferably derived from
XX the wild-type pokeweed Antiviral Protein (PAP) (AAR57152).
XX Specifically, the mutants are PAP1 (with gly replacing wild-type
XX Arg at position 68) and PAP9 (with Tyr replacing wild-type Phe and
XX Arg replacing wild-type Lys at positions 196 and 211, respectively).
XX
XX Sequence 292 AA:

Query Match 72.48; Score 1170.5; DB 15; Length 292;
Best Local Similarity 77.08; Pred. No. 2.3e-105;
Matches 224; Conservative 30; Mismatches 36; Indels 1; Gaps 1;
Qy 25 INTITFDAGNATINKYATFMESLRNQAKDKPKCYGIPMLPDTNSTPKYLLVKGANLX 84
Db 2 VNTIYVVGSTTISKYATFLNDRNEAKDPSLKYGIPMLPNTNPKYLVVLOGSNKK 61
Qy 85 TITLMLRRNNLYVMGSDPPFNKCRHYHFNIDTSTERTDVENTLCSRSSRVAMSYN 144
Db 62 TITLMLRRNNLYVMGSDPPFNKCRHYHFNIDISGTERQDVTTLCPNANSKVNINFD 121
Qy 145 SLYPTMEKKAQVNSRNOVOLGQIOLSSDICKISQVSDPPVKTEAFFLVAIOMVSEAKF 204
Db 122 SRYPTLESKAGVRSQVQLGQIOLDSNIGKISGVMSFTEKTEAEFLVLAIOMVSEAKF 181
Qy 205 KYIENQVKTENRFAFYDPKVINLEEKWGIKISEAHNAKNGALPKPLVDKAGTKWIVL 264
Db 182 KYIENQVKTENRFAFNPNKVLNLQETWGIKISTAJHDAKNGVLPKPLVDASGAKWIVL 241
Qy 265 KVDEINRDVALLKYVNGTCQTTY-ONAMFSQVILSTYYNYSNLGDLFEFG 314
Db 242 KVDEIKPDVALLNVVGGSCQTTYQNAMFPOLIMSTYYNYSNLGDLFEFG 292
RESULT 5
AAR57154
ID AAR57154 standard; protein: 292 AA.
XX AAR57154;
XX

Printed 11/17/2004

SRNT

PT viruses and/or fungi -
XX Examples: Page 4-5: 43pp: English.
XX This is the pokeweed antiviral protein (PAP) amino acid sequence. PAP is
CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
CC catalytically removes a specific adenine residue from a highly conserved
CC stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
CC antiviral protein II (PAP II) protein confers antiviral and/or antifungal
CC activities to plants. A DNA molecule encoding a PAP II protein with an
CC intact catalytic active site amino acid residue (E172) is useful for
CC generating transgenic plants. PAP II DNA is useful for generating a
CC protoplast or introducing the DNA directly into a plant part prior to
CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
CC activity thus have increased resistance to viruses and/or fungi. Viruses
CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
CC other plants pests including insects, bacteria and nematodes. PAP II DNA
CC is also useful for identifying a PAP II protein having reduced
CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC unlike PAP transgenic plants which are stunted and sterile, PAP II
CC transgenic plants have a normal and fertile phenotype.
XX Sequence 313 AA:

Query Match 76.4% Score 1235.5; DR 21; Length 313;
Best Local Similarity 75.9%; Pred. No. 1.2e-111;
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;
Oy 1 MKVMLVVVVTLLIAALPTSTCAINTITFDAGNATINKYATFESLRNOAKDKPKCYG 60
Db 1 MKSMLVVTISI--WLLIAPTSTWAVNTIYVNGSTTISKYATFLNDRNEAKDPSLACYG 58
Oy 61 IPMPLDNTNPKYLLVKGLOGANIKTITLMLRRNNLYVMGYSDDPFGNKKRYHFNIDTST 120
Db 59 IPMPLDNTNPKYLLVKGLOGANIKTITLMLRRNNLYVMGYSDDPFGNKKRYHFNIDTST 118
Oy 121 ERTDVENTLCSSSSSRVAMSTNYSLYPTMEKKAEVNSRNQVGLQIQLSSDICKISGV 180
Db 119 ERQDVETTLCPNANSRVSKNINFSRYPTLESKAGVRSQVQLC1Q1LDSNICKISGV 178
Oy 181 SFPVKTEAFFLLVAIONVSEARFKYIENQVKTNFNRAFYDPKPVINLEEKWKISETAIH 240
Db 179 SFTKTEAEFLVAIONVSEARFKYIENQVKTNFNRAFYDPKPVINLEEKWKISETAIH 238
Oy 241 NAKNCALPKPLELVDAGKTKWILRVDEINRDVALLKYVNGTCQTTY-ONAMFSOVITST 299
Db 239 DAKNGVLPKPLELVDAGKTKWILRVDEIKPDVALLKYVNGTCQTTYONAMFPOLTINST 298
Oy 300 YNYMNSLGDLEFGF 314
Db 299 YNYMNSLGDLEFGF 313

RESULT 2
AAB36500 standard: Protein: 313 AA.
XX AAB36500:
XX AAB36500:
XX 06-MAR-2001 (first entry)
XX Phytolacca americana pokeweed antiviral protein SEQ ID NO:2.
XX Phytolacca americana; pokeweed; pokeweed; pokeweed antiviral protein: PAP;
KW cancer; biotrophic; fusion protein; immunoconjugate; mutant;
KW cytostatic; anti-Hiv; human immunodeficiency virus; AIDS; leukaemia;
KW lymphoma; brain tumour; neuroblastoma; soft tissue sarcoma;
KW osteosarcoma.
XX

OS Phytolacca americana.
XX US6146628-A.
XX 14-NOV-2000.
XX 11-JUL-1995: 95US-0501253.
XX 11-JUL-1995: 95US-0501253.
PR (MINU) UNIV MINNESOTA & RUTGERS.
PA (UYNE-) UNIV STATE NEW JERSEY.
XX Uckun FM, Tumor NE;
XX WPI: 2001-040422/05.
DR N-PSDB: MAC87929.
XX Immunoconjugates useful for treating cancer and acquired
PT immunodeficiency syndrome, comprises mutant pokeweed anti-viral protein
PT and a targeting moiety that binds a cell surface receptor
XX Example 6: Column 49-52: 32pp: English.
XX The present invention describes a fusion protein or an immunoconjugate
CC (1), comprising mutant pokeweed Anti-viral Protein (PAP) having an
CC amino acid substitution at residue 75, 97 or 176 of native PAP and a
CC targeting moiety that binds a cell surface receptor. (1) can have
CC cytotoxic and anti-Hiv activities, and is an inhibitor of cellular
CC RNA or protein synthesis. (1) is useful for treating AIDS and cancers
CC including leukaemia, lymphoma, a brain tumour, neuroblastoma,
CC osteosarcoma, soft tissue sarcoma, breast, prostate, ovarian,
CC testicular, melanoma, lung, or colon cancer. Immunoconjugates prepared
CC using PAP mutants exhibit an improved therapeutic index over
CC immunoconjugates containing either wild-type PAP or variant PAP.
CC The present sequence represents the wild-type PAP, which is given in
CC the exemplification of the present invention.
XX Sequence 313 AA:

Query Match 76.4% Score 1232.5; DR 22; Length 313;
Best Local Similarity 75.6%; Pred. No. 2.4e-111;
Matches 238; Conservative 34; Mismatches 40; Indels 3; Gaps 2;
Oy 1 MKVMLVVVVTLLIAALPTSTCAINTITFDAGNATINKYATFESLRNOAKDKPKCYG 60
Db 1 MKSMLVVTISI--WLLIAPTSTWAVNTIYVNGSTTISKYATFLNDRNEAKDPSLACYG 58
Oy 61 IPMPLDNTNPKYLLVKGLOGANIKTITLMLRRNNLYVMGYSDDPFGNKKRYHFNIDTST 120
Db 59 IPMPLDNTNPKYLLVKGLOGANIKTITLMLRRNNLYVMGYSDDPFGNKKRYHFNIDTST 118
Oy 121 ERTDVENTLCSSSSSRVAMSTNYSLYPTMEKKAEVNSRNQVGLQIQLSSDICKISGV 180
Db 119 ERQDVETTLCPNANSRVSKNINFSRYPTLESKAGVRSQVQLC1Q1LDSNICKISGV 178
Oy 181 SFPVKTEAFFLLVAIONVSEARFKYIENQVKTNFNRAFYDPKPVINLEEKWKISETAIH 240
Db 179 SFTKTEAEFLVAIONVSEARFKYIENQVKTNFNRAFYDPKPVINLEEKWKISETAIH 238
Oy 241 NAKNCALPKPLELVDAGKTKWILRVDEINRDVALLKYVNGTCQTTY-ONAMFSOVITST 299
Db 239 DAKNGVLPKPLELVDAGKTKWILRVDEIKPDVALLKYVNGTCQTTYONAMFPOLTINST 298
Oy 300 YNYMNSLGDLEFGF 314
Db 299 YNYMNSLGDLEFGF 313

RESULT 3
AAB48548 standard: Protein: 313 AA.
XX AAB48548
XX

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 28, 2003, 09:45:44 : Search time 76 Seconds
(without alignments)
550.535 Million cell updates/sec

Title: US-09-978-274A-2

Perfect score: 1617

Sequence: 1 MKVMLVVVVTIAWLAIAAPT.....VIISTYNYNMLGDLFEGF 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*
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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1235.5	76.4	313	21 AAY58025	Wild-type pokeweed
2	1232.5	76.2	313	22 AAB36500	Phytolacca americana
3	1229.5	76.0	313	15 AAR48548	Sequence of Phytol
4	1170.5	72.4	292	15 AAR57152	Wild-type Pokeweed
5	1164.5	72.0	292	15 AAR57154	Pokeweed Antiviral
6	1163.5	72.0	292	15 AAR57153	Pokeweed Antiviral
7	1160.5	71.8	292	15 AAW26773	Phytolacca insular
8	1147.5	71.0	315	19 AAW26774	Phytolacca insular
9	1147.5	71.0	315	20 AAW51033	Phytolacca insular
10	1113.5	68.9	294	14 AAR37345	Pokeweed antiviral

11	1096.5	67.8	261	12 AAR13112	Anti-viral protein
12	1096.5	67.8	261	16 AAR74184	Type I RIP pokewee
13	1096.5	67.8	261	18 AAR25145	PAP-S (a ribosome
14	1096.5	67.8	261	18 AAR21708	PAP-S RIP. Phytol
15	1089.5	67.4	261	14 AAR37298	Plant type I RIP p
16	1089.5	67.4	261	16 AAR63910	Type I ribosome-in
17	1047	64.7	261	18 AAW14218	Mature pokeweed an
18	1046	64.7	262	18 AAW14164	Mature pokeweed an
19	1043	64.5	262	18 AAW14256	Mature pokeweed an
20	1041	64.4	260	18 AAW14219	Mature pokeweed an
21	1041	64.4	262	18 AAW14163	Mature pokeweed an
22	1036	64.1	259	18 AAW14220	Mature pokeweed an
23	1033	63.9	257	18 AAW14222	Mature pokeweed an
24	1033	63.9	258	18 AAW14221	Mature pokeweed an
25	1031	63.8	305	15 AAR54839	Antiviral protein
26	1030	63.7	256	18 AAW14223	Mature pokeweed an
27	1029	63.6	254	18 AAW14225	Mature pokeweed an
28	1029	63.6	255	18 AAW14224	Mature pokeweed an
29	1025	63.4	305	16 AAR80106	P. insularis antiv
30	1023	63.3	253	18 AAW14226	Mature pokeweed an
31	1022	63.2	251	18 AAW14228	Mature pokeweed an
32	1022	63.2	252	18 AAW14227	Mature pokeweed an
33	1017	62.9	250	18 AAW14229	Mature pokeweed an
34	1013	62.6	249	18 AAW14230	Mature pokeweed an
35	1012	62.6	248	18 AAW14231	Mature pokeweed an
36	1007	62.3	247	18 AAW14232	Mature pokeweed an
37	1000	61.8	246	18 AAW14233	Mature pokeweed an
38	996	61.6	245	18 AAW14234	Mature pokeweed an
39	991	61.3	244	18 AAW14235	Mature pokeweed an
40	985	60.9	243	18 AAW14236	Mature pokeweed an
41	983	60.8	240	18 AAW14239	Mature pokeweed an
42	983	60.8	241	18 AAW14238	Mature pokeweed an
43	983	60.8	242	18 AAW14237	Mature pokeweed an
44	979	60.5	239	18 AAW14240	Mature pokeweed an
45	974	60.2	238	18 AAW14241	Mature pokeweed an

ALIGNMENTS

RESULT 1

AAY58025

ID AAY58025 standard; Protein: 313 AA.

XX AAY58025;

XX 29-FEB-2000 (first entry)

XX Wild-type pokeweed antiviral protein (PAP) amino acid sequence.

XX Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;

XX ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;

XX potato virus X; cucumber mosaic virus; CMV;

XX tomato yellow leaf curl virus.

XX Phytolacca americana.

OS Phytolacca americana.

PN WO9960843-A1.

XX 02-DEC-1999.

XX 21-MAY-1999; 99MO-US11301.

XX 22-MAY-1998; 98US-0086374.

XX (RUTF) UNIV KUTGERS STATE NEW JERSEY.

XX Tumer NE, Wang P;

XX WPI; 2000-062555/05.

XX N-PSDR; AAZ45197.

XX New antiviral DNA useful for generating transgenic plants resistant to

Query Match 2.38; Score 22; DB 1; Length 918;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 GTGATGGCTATTCTGATCCCT 310
|||||
DB 277 GTGATGGCTATTCTGATCCCT 298

RESULT 14

US-08-996-441B-51/C
; Sequence 51, Application US/08996441B

; Patent No. 6023013

; GENERAL INFORMATION:

; APPLICANT: English, Leigh H.

; APPLICANT: Brussock, Susan M.

; APPLICANT: Malvar, Thomas M.

; APPLICANT: Bryson, James W.

; APPLICANT: Kulesza, Caroline A.

; APPLICANT: Walters, Frederick S.

; APPLICANT: Slatin, Stephen L.

; APPLICANT: Von Tersch, Michael A.

; APPLICANT: Romano, Charles

; TITLE OF INVENTION: INSECT-RESISTANT TRANSGENIC PLANTS

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/996.441B

; FILING DATE: 18-DEC-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: MECO:151

; TELEPHONE: 512/418-3000

; TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 51:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1956 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1953

; US-08-996-441B-51

Query Match 2.18; Score 20; DB 3; Length 1956;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 ACTTCAACTTGTGCGCATAAA 77
|||||
DB 344 ACTTCAACTTGTGCGCATAAA 325

RESULT 15

US-08-996-441B-55/C

; Sequence 55, Application US/08996441B

; Patent No. 6023013

; GENERAL INFORMATION:

06/02/2003

93

09978274

SRNI

Printed 11/17/2004

TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 2.3%, Score 22; DB 1: Length 918;
Best Local Similarity 100.0%; Pred. NO. 0.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 289 GTGATGGGCTATTCTGATCCCT 310
Db 277 GTGATGGGCTATTCTGATCCCT 298

RESULT 12
US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
NUMBER OF SEQUENCES: 4
TITLE OF INVENTION: Transgenic Plant
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/0A445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Query Match 2.3%, Score 22; DB 1: Length 918;
Best Local Similarity 100.0%; Pred. NO. 0.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 289 GTGATGGGCTATTCTGATCCCT 310
Db 277 GTGATGGGCTATTCTGATCCCT 298

RESULT 13
US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 5723326
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: NO. 5723326el Genome Coding Phytolacca Antiviral
NUMBER OF SEQUENCES: 2
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

APPLICANT: Tumer, Nilgun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501.253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225...1163
US-08-501-253A-1

Query Match 3.1% Score 29: DB 3: Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Oy 915 TAATCTGGTGATCTATTTCAGGATTCT 943
|||||
Db 1136 TAATCTGGTGATCTATTTCAGGATTCT 1164
RESULT 10
PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Poxweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/500,594
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225...1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1
Query Match 3.1% Score 29: DB 5: Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Oy 915 TAATCTGGTGATCTATTTCAGGATTCT 943
|||||
Db 1136 TAATCTGGTGATCTATTTCAGGATTCT 1164
RESULT 11
US-08-138-636-1
Sequence 1, Application US/08138636
Patent No. 5348865
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seon
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5348865el Genome Coding Phytolacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700

Rest Local Similarity 100.0%; Pred. No. 3e-05; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTTGGTGATCTATTGAAGGATTCT 943
DB 1136 TAATCTTGGTGATCTATTGAAGGATTCT 1164

RESULT 7
US-09-005-273-1
Sequence 1, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005.273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500.611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500.694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-1

Query Match 3.1%; Score 29; DB 3; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTTGGTGATCTATTGAAGGATTCT 943
DB 1136 TAATCTTGGTGATCTATTGAAGGATTCT 1164

09978274

SRNI

Printed 11/17/2004

RESULT 8
US-09-005-273-3
Sequence 3, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005.273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500.611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500.694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3

Query Match 3.1%; Score 29; DB 3; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTTGGTGATCTATTGAAGGATTCT 943
DB 1136 TAATCTTGGTGATCTATTGAAGGATTCT 1164

RESULT 9
US-09-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih

09978274

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1

Query Match 3.1% Score 29; DB 2; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTTCAGGATTCT 943
Db 1136 TAATCTGGTGATCTATTTCAGGATTCT 1164

RESULT 5
US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BR4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

06/02/2003

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-865-169-1

Query Match 3.1% Score 29; DB 3; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTTCAGGATTCT 943
Db 1136 TAATCTGGTGATCTATTTCAGGATTCT 1164

RESULT 6
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BR4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-865-169-2

Query Match 3.1% Score 29; DB 3; Length 1379;

ORGANISM: Phytolacca americana
TISSUE TYPE: Leaf
US-08-373-858-1

Query Match 3.1%; Score 29; DB 1; Length 1195;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTGAAGGATTCT 943
|||||
DB 944 TAATCTGGTGATCTATTGAAGGATTCT 972
|||||

RESULT 2

US-08-342-786B-1
Sequence 1, Application US/08342786B
Patent No. 5648234

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

APPLICANT: Choi, Kyu-Whan

APPLICANT: Lee, Kwan-Ho

APPLICANT: Kim, Man-Keun

TITLE OF INVENTION: Antiviral Protein

TITLE OF INVENTION: Antiviral Protein

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby

STREET: 805 Third Ave.

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,786B

FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/147,024

FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08862-US1

TELEPHONE: (212)527-7700

TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ANTI-SENSE: NO

ORGANISM: Phytolacca americana L.

IMMEDIATE SOURCE:

CLONE: P4P

US-08-342-786B-1

Query Match 3.1%; Score 29; DB 1; Length 1195;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTGAAGGATTCT 943

DB 944 TAATCTGGTGATCTATTGAAGGATTCT 972
|||||

RESULT 3

US-08-500-611-1

Sequence 1, Application US/08500611

Patent No. 5756322

GENERAL INFORMATION:

APPLICANT: Turner, Nilgun E.

TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik

STREET: 600 South Avenue West

CITY: Westfield

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/500,611

FILING DATE: 11-JUL-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REFERENCE/DOCKET NUMBER: OCIRS 3.0-034

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5060

TELEFAX: 908-654-7866

TELEX: 139-125

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 225..1163

FEATURE:

NAME/KEY: mutation

LOCATION: replace(233, "a")

FEATURE:

NAME/KEY: mutation

LOCATION: replace(349, "g")

FEATURE:

NAME/KEY: mutation

LOCATION: replace(435, "c")

US-08-500-611-1

Query Match 3.1%; Score 29; DB 1; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTGAAGGATTCT 943
|||||

DB 1136 TAATCTGGTGATCTATTGAAGGATTCT 1164
|||||

RESULT 4

US-08-500-694-1

Sequence 1, Application US/08500694

Patent No. 580329

GENERAL INFORMATION:

APPLICANT: Turner, Nilgun E.

TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein

NUMBER OF SEQUENCES: 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 03:32:48 : Search time 63 seconds
(without alignments)
4600.151 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

Sequence: 1 atgaaggtgatctttagt.....atctattgaagattctaa 945

Scoring table: OLIGO-NUC

Gapop 60.0, Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 802724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- Issued_Patents_NA:*
- 1: /cgn2.6/ptodata/1/ina/5A_COMB.seq:*
 - 2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
 - 3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq:*
 - 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	3.1	1195	1	US-08-373-858-1
2	29	3.1	1195	1	US-08-342-786B-1
3	29	3.1	1379	2	US-08-500-611-1
4	29	3.1	1379	2	US-08-500-694-1
5	29	3.1	1379	3	US-07-865-169-1
6	29	3.1	1379	3	US-07-865-169-2
7	29	3.1	1379	3	US-09-005-273-1
8	29	3.1	1379	3	US-09-005-273-3
9	29	3.1	1379	3	US-08-501-253A-1
10	29	3.1	1379	5	PCT-US96-11546-1
11	22	2.3	918	1	US-08-138-636-1
12	22	2.3	918	1	US-08-319-622A-1
13	22	2.3	918	1	US-08-471-564-1
14	20	2.1	1956	3	US-08-996-441B-51
15	20	2.1	1956	3	US-08-996-441B-55
16	20	2.1	1956	3	US-08-996-441B-57
17	20	2.1	1956	3	US-08-993-722A-51
18	20	2.1	1956	3	US-08-993-722A-55
19	20	2.1	1956	3	US-08-993-722A-57
20	20	2.1	1956	3	US-08-993-170A-51
21	20	2.1	1956	3	US-08-993-170A-55
22	20	2.1	1956	3	US-08-993-170A-57
23	20	2.1	1956	3	US-08-993-775B-51
24	20	2.1	1956	3	US-08-993-775B-55
25	20	2.1	1956	3	US-08-993-775B-57
26	20	2.1	1959	3	US-08-996-441B-1
27	20	2.1	1959	3	US-08-996-441B-3

c 28	20	2.1	1959	3	US-08-996-441B-5	Sequence 5, Appl
c 29	20	2.1	1959	3	US-08-996-441B-7	Sequence 7, Appl
c 30	20	2.1	1959	3	US-08-996-441B-9	Sequence 9, Appl
c 31	20	2.1	1959	3	US-08-996-441B-11	Sequence 11, Appl
c 32	20	2.1	1959	3	US-08-996-441B-13	Sequence 13, Appl
c 33	20	2.1	1959	3	US-08-996-441B-15	Sequence 15, Appl
c 34	20	2.1	1959	3	US-08-996-441B-17	Sequence 17, Appl
c 35	20	2.1	1959	3	US-08-996-441B-19	Sequence 19, Appl
c 36	20	2.1	1959	3	US-08-996-441B-21	Sequence 21, Appl
c 37	20	2.1	1959	3	US-08-996-441B-23	Sequence 23, Appl
c 38	20	2.1	1959	3	US-08-996-441B-25	Sequence 25, Appl
c 39	20	2.1	1959	3	US-08-996-441B-27	Sequence 27, Appl
c 40	20	2.1	1959	3	US-08-996-441B-29	Sequence 29, Appl
c 41	20	2.1	1959	3	US-08-996-441B-31	Sequence 31, Appl
c 42	20	2.1	1959	3	US-08-996-441B-33	Sequence 33, Appl
c 43	20	2.1	1959	3	US-08-996-441B-35	Sequence 35, Appl
c 44	20	2.1	1959	3	US-08-996-441B-37	Sequence 37, Appl
c 45	20	2.1	1959	3	US-08-996-441B-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-08-373-858-1
Sequence 1, Application US/08373858
Patent No. 5633155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwan-Ho
APPLICANT: Na, Byeong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytolacca
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 4A5
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match 20.1% Score 325; DB 10; Length 332;
Best Local Similarity 32.4%; Pred. No. 6e-22;
Matches 88; Conservative 50; Mismatches 112; Indels 22; Gaps 8;
QY 15 LIAPTSTCAINTITFDAGNATINKYATFMESLRNOAKDPKLCYIGPMLPDTNSTPK-- 72
DB 14 LLAAPAMAGLOTVSFSTKGATYYTVNLFNLRLVKLK-PEGNSHGIGPLRLKKCDOPGKC 72
QY 73 YLLVLOGANLKITILMLRNNLYVMGYSDPENGKCRHYHFNITSTERTDV-ENTLCS 131
DB 73 FVLVALSNDGOLAEIAIDVTSVYVGYQ-----VNRSYFFKADAPDAAYEGLEFKNT--- 124
QY 132 SSSSRVAMSYNTSLPTMEKKAENVSRNOVGLGILSSDICKI--SGVDSFPVKTEAF 189
DB 125 -----IKRLHGGTYPSLE--GEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETAS 177
QY 190 FLVVAIQVSEARFYENQVKTENRNFYDPKVINLEEKWKGTISEAH-NAKNGALP 248
DB 178 SLVVIQVSEARFYENQVKTENRNFYDPKVINLEEKWKGTISEAH-NAKNGALP 248
QY 249 KPLELVDAGKTWILVRVDEINRDVALLKVN 280
DB 238 EAVELERANGKYYVTAVDQVXPKIALAKFVD 269

RESULT 14
US-09-765-527-247
Sequence 247, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247

Query Match 19.3% Score 312; DB 10; Length 251;
Best Local Similarity 32.4%; Pred. No. 6.4e-21;
Matches 85; Conservative 48; Mismatches 107; Indels 22; Gaps 8;
QY 25 INTITFDAGNATINKYATFMESLRNOAKDPKLCYIGPMLPDTNSTPK--YLLVLOGAN 82
DB 2 LQTVSFSTKGATYYTVNLFNLRLVKLK-PEGNSHGIGPLRLKKCDOPGKCFCFVLVALSWDN 60
QY 83 LKTTITMLRNNLYVMGYSDPENGKCRHYHFNITSTERTDV-ENTLCSSSSSSKVAMSI 141
DB 61 GOLAEIAIDVTSVYVGYQ-----VNRSYFFKADAPDAAYEGLEFKNT-----IKRLK 107
QY 142 NYSNLYPTMEKKAENVSRNOVGLGILSSDICKI--SGVDSFPVKTEAFLLVVAIQVVS 199
DB 108 HFGGTYPSLE--GEKAYRETTDLGIEPLRIGIKKLDENAIIDNYKPTETASLLVVIQVVS 165
QY 200 EAARKFYENQVKTENRNFYDPKVINLEEKWKGTISEAH-NAKNGALPDKPILVLDAGK 258
DB 166 EAARTFYENQVKTENRNFYDPKVINLEEKWKGTISEAH-NAKNGALPDKPILVLDAGK 258
QY 259 TKWILVRVDEINRDVALLKVN 280
DB 226 KKYVTVAVDQVXPKIALAKFVD 247

RESULT 15
US-09-792-793A-36
Sequence 36, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
FILE REFERENCE: 25020-601D
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 250
TYPE: PRT
ORGANISM: Momordica charantia
US-09-792-793A-36

Query Match 16.1% Score 261; DB 9; Length 250;
Best Local Similarity 32.6%; Pred. No. 3.3e-16;
Matches 86; Conservative 41; Mismatches 117; Indels 20; Gaps 10;
QY 18 APTSTCAINTITFDAGNATINKYATFMESLRNOAKDPKLCYIGPMLPDTNSTPKYLLV 76
DB 3 APT-----LETIASLUNNPT--TYISFNTNITKVADKTEQC-TTQIKSKT-FTQKYSVI 52
QY 77 KLGANLKITILMLRNNLYVMGYSDPENGKCRHYHFNITSTERTDV-ENTLCSSSSKR 136
DB 53 DLIVSSTQKITIALDMADLYLVGYSDIAN-NKGRAFFEDVTEA----VANNEFFVATCT 107
QY 137 VAMSYNLYPTMEKKAENVSRNOVGLGILSSDICKIQTSLSSDICKISGVDSFPVKTEAFLLVVAIQ 196
DB 108 NKIKLTFTGSGYDLEKNGCLRKDN--PLGIVRLNSIVNIYG-KAGDVKKQAKFFLLAIQ 164

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match 20.1% Score 325; DB 10; Length 293;
Best Local Similarity 32.4% Pred. No. 5e-22;
Matches 88; Conservative 50; Mismatches 112; Indels 22; Gaps 8;
QY 15 LIAAPTSTCAINTITFDAGNATINKYATFMESLRNOAKPKLKCYGIPMLPDTNSTPK-- 72
DB 14 LLAQAQAMAGLDTVSFSTKGATITVYVNFNLRLVKLK-PEGNSHGIPLLRKKCDPGKC 72
QY 73 YLLVKLOGANLKTITLMLRNLNLYGVSDPFGNGKCRYHIFNDITSTERTD-ENTLCS 131
DB 73 FVLVLSNDNGQLAEIAIDVTSVYVGYQ-----VNRSYFFKADDAAYEGLFKNT--- 124
QY 132 SSSSRVAMSYNLSYPTMEKKAENSRNOVQIGIQLSSDICKI--SGVDSFPVKTEAF 189
DB 125 -----IKTRLHFGGTYPSLE--GEKAYRETTDLGIRLIGIKKLDENATDNYKPTETAS 177
QY 190 FLVVAIQWSEARFKYIENQVKTENRATYDPKPKVINLEKKGKISEATH-NAKNGALP 248
DB 178 SLVVQIQWSEARFTFIENQIRNFQOIRPANNITISLENKWKLSFQIRTSGANGMFS 237
QY 249 KPLELDVAKGKTWILVRVDEINRQVALLKYVN 280
DB 238 EAVELERANGKKYVTVAVDQVQPKIALLEKFD 269

RESULT 12
US-09-765-527-253
Sequence 253, Application US/09765527
Patent No. US2002000638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-765-527-253

Query Match 20.1% Score 325; DB 10; Length 309;
Best Local Similarity 32.4% Pred. No. 5.4e-22;
Matches 88; Conservative 50; Mismatches 112; Indels 22; Gaps 8;
QY 15 LIAAPTSTCAINTITFDAGNATINKYATFMESLRNOAKPKLKCYGIPMLPDTNSTPK-- 72
DB 14 LLAQAQAMAGLDTVSFSTKGATITVYVNFNLRLVKLK-PEGNSHGIPLLRKKCDPGKC 72
QY 73 YLLVKLOGANLKTITLMLRNLNLYGVSDPFGNGKCRYHIFNDITSTERTD-ENTLCS 131
DB 73 FVLVLSNDNGQLAEIAIDVTSVYVGYQ-----VNRSYFFKADDAAYEGLFKNT--- 124
QY 132 SSSSRVAMSYNLSYPTMEKKAENSRNOVQIGIQLSSDICKI--SGVDSFPVKTEAF 189
DB 125 -----IKTRLHFGGTYPSLE--GEKAYRETTDLGIRLIGIKKLDENATDNYKPTETAS 177
QY 190 FLVVAIQWSEARFKYIENQVKTENRATYDPKPKVINLEKKGKISEATH-NAKNGALP 248
DB 178 SLVVQIQWSEARFTFIENQIRNFQOIRPANNITISLENKWKLSFQIRTSGANGMFS 237
QY 249 KPLELDVAKGKTWILVRVDEINRQVALLKYVN 280
DB 238 EAVELERANGKKYVTVAVDQVQPKIALLEKFD 269

RESULT 13
US-09-765-527-251
Sequence 251, Application US/09765527
Patent No. US2002000638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

LENGTH: 275
TYPE: PRT
ORGANISM: Saponaria officinalis
US-09-792-793A-35

Query Match 21.2% Score 342; DB 9; Length 275;
Best Local Similarity 35.9% Pred. No. 1.6e-23;
Matches 94; Conservative 51; Mismatches 97; Indels 20; Gaps 9;

Qy 25 INTITDAGNATINKYATFMSLRNQAOKPKLKYGIPM-LPDTNSTPKYLLVKGANL 83
Db 1 VTSITDLVNPTAGQYSSFDKIRNNVKDPNLYGGTDIAVIGPPSKKELRINFQSSR- 59
Qy 84 KTTLMRLNNLYVMGYSDPFNGKCR-YHIFNDITSTERTDVENTLCSSSSSRVAMSN 142
Db 60 GTVSLGLKRONLYVAYLAMDNTNVRAYYRSEITSAEST-ALFPEATTAQNAKALE 115
Qy 143 YNSLYPTMEKKAQV-NSRNOVOLGIOLSSDICKISGVDSFPVKTEAFFLLVATOMV 198
Db 116 YTEDYOSIEKNAQITQGDOSRKELGLDLSSTMEAVN-KKARVVKDEARFLIAIOMT 174
Qy 199 SEARFKYIENOVKTNFRAYPDPKVINLEEKWGISIAIH-NAKNGALPKPLELVDK 257
Db 175 AEAAFRYIQLVKNFKNSENKVIQFEVNNKKISTAIYGDKNGVFNKDYDFGFK 234
Qy 258 GTKWIVLRVDEINRDVALLKYV 279
Db 235 -----VRQVKDL--QMGLLMYL 249

RESULT 9
US-09-792-793A-79

Sequence 79, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 79
LENGTH: 327
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protein
OTHER INFORMATION: 1-Beta-AM-SAPORIN
US-09-792-793A-79

Query Match 21.2% Score 342; DB 9; Length 327;
Best Local Similarity 35.9% Pred. No. 1.6e-23;
Matches 94; Conservative 51; Mismatches 97; Indels 20; Gaps 9;
Qy 25 INTITDAGNATINKYATFMSLRNQAOKPKLKYGIPM-LPDTNSTPKYLLVKGANL 83
Db 75 VTSITDLVNPTAGQYSSFDKIRNNVKDPNLYGGTDIAVIGPPSKKELRINFQSSR- 133
Qy 84 KTTLMRLNNLYVMGYSDPFNGKCR-YHIFNDITSTERTDVENTLCSSSSSRVAMSN 142
Db 134 GTVSLGLKRONLYVAYLAMDNTNVRAYYRSEITSAEST-ALFPEATTAQNAKALE 189
Qy 143 YNSLYPTMEKKAQV-NSRNOVOLGIOLSSDICKISGVDSFPVKTEAFFLLVATOMV 198
Db 190 YTEDYOSIEKNAQITQGDOSRKELGLDLSSTMEAVN-KKARVVKDEARFLIAIOMT 248
Qy 199 SEARFKYIENOVKTNFRAYPDPKVINLEEKWGISIAIH-NAKNGALPKPLELVDK 257
Db 249 AEAAFRYIQLVKNFKNSENKVIQFEVNNKKISTAIYGDKNGVFNKDYDFGFK 308

Qy 258 GTKWIVLRVDEINRDVALLKYV 279
Db 309 -----VRQVKDL--QMGLLMYL 323

RESULT 10
US-09-792-793A-76

Sequence 76, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 76
LENGTH: 332
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion
OTHER INFORMATION: MCH3-AM-SAPORIN
US-09-792-793A-76

Query Match 21.2% Score 342; DB 9; Length 332;
Best Local Similarity 35.9% Pred. No. 1.6e-23;
Matches 94; Conservative 51; Mismatches 97; Indels 20; Gaps 9;

Qy 25 INTITDAGNATINKYATFMSLRNQAOKPKLKYGIPM-LPDTNSTPKYLLVKGANL 83
Db 80 VTSITDLVNPTAGQYSSFDKIRNNVKDPNLYGGTDIAVIGPPSKKELRINFQSSR- 138
Qy 84 KTTLMRLNNLYVMGYSDPFNGKCR-YHIFNDITSTERTDVENTLCSSSSSRVAMSN 142
Db 139 GTVSLGLKRONLYVAYLAMDNTNVRAYYRSEITSAEST-ALFPEATTAQNAKALE 194
Qy 143 YNSLYPTMEKKAQV-NSRNOVOLGIOLSSDICKISGVDSFPVKTEAFFLLVATOMV 198
Db 195 YTEDYOSIEKNAQITQGDOSRKELGLDLSSTMEAVN-KKARVVKDEARFLIAIOMT 254
Qy 199 SEARFKYIENOVKTNFRAYPDPKVINLEEKWGISIAIH-NAKNGALPKPLELVDK 257
Db 254 AEAAFRYIQLVKNFKNSENKVIQFEVNNKKISTAIYGDKNGVFNKDYDFGFK 314
Qy 258 GTKWIVLRVDEINRDVALLKYV 279
Db 314 -----VRQVKDL--QMGLLMYL 328

RESULT 11
US-09-765-527-259

Sequence 259, Application US/09765527
Patent No. US20020008638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Hornum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-8402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 332
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-Loxin fusion protein
OTHER INFORMATION: MCP1-AM-SAPORIN
US-09-792-793A-73

Query Match 21.4% Score 346; DB 9; Length 332;
Best Local Similarity 35.8% Pred. No. 6.9e-24;
Matches: 95; Conservative 51; Mismatches 96; Indels 20; Gaps 9;

QY 22 TCAINTITDAGNATINKYATFMSLRNOAKDPKLCYGPW-LPDNSTPKYLLVKLQC 80
DB 77 TAMVTSITLDVNPAGQYSSFDKIRNNVKDPNLYGCTDAVIGPPSKKFLRNFOS 136
QY 81 ANLKTITLRRNNLYVMGYSDPPFNGKCR-YHIFNDITSTERTDVENTLCSSSSRVAM 135
DB 137 SR-GTVSLGKRDNLVYVAYLAMDTNVRNRYFRSEITSAST-----ALFPEATANOK 191
QY 140 SINNSLYPTMEKAEV-----NSRNQVQIGTIOILSSDICKISCVSPFPVKTAEFFLLV 195
DB 192 ALEYTEDYOSIEKNAQITOGDOSRKELGIDLLSTSMCAVN-KKARVVKDEARFLLAI 250
QY 196 QNVSEARKEYTENQVTFNRAFYDPKVINIEKWKISAEIH-NAKNGALPKPLFLVIAK 254
DB 251 QMTAEARERYIQNLVIRKPNFNSKNVIOFVNNKKISTAIYGDAGKNGVFNKIDYDFG 310
QY 255 DAKGTWIVLRVDEINROVALLKYV 279
DB 311 FGK-----VRQVKDL--QMGLLYL 328

RESULT 6
US-09-792-793A-82
Sequence 82, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 330
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-Loxin fusion protein
OTHER INFORMATION: EOTAXIN-AM-SAPORIN
US-09-792-793A-82

Query Match 21.2% Score 343.5; DB 9; Length 330;
Best Local Similarity 35.9% Pred. No. 1.2e-23;
Matches: 97; Conservative 52; Mismatches 100; Indels 21; Gaps 10;
QY 18 APTSTCA-INTITDAGNATINKYATFMSLRNOAKDPKLCYGPW-LPDNSTPKYLL 75
DB 70 SPTPKAMVTSITLDVNPAGQYSSFDKIRNNVKDPNLYGCTDAVIGPPSKKFLR 129
QY 76 VKLOGANKTITLRRNNLYVMGYSDPPFNGKCR-YHIFNDITSTERTDVENTLCSSSS 134
DB 130 INFOSSR-GTVSLGKRDNLVYVAYLAMDTNVRNRYFRSEITSAST-----ALFPEAT 184
QY 135 SRVAMTSINNSLYPTMEKAEV-----NSRNQVQIGTIOILSSDICKISGVDSFPVKTAEFF 190

DB 185 TANQKALEYTTEDYOSIEKNAQITOGDOSRKELGIDLLSTSMCAVN-KKARVVKDEARF 243
QY 191 LLVATQMVSEARKEYTENQVTFNRAFYDPKVINIEKWKISAEIH-NAKNGALPK 249
DB 244 LLJAJQMTAEARERYIQNLVIRKPNFNSKNVIOFVNNKKISTAIYGDAGKNGVFNK 303
QY 250 PLELVDAKGTWIVLRVDEINROVALLKYV 279
DB 304 DYDFGFGK-----VRQVKDL--QMGLLYL 326

RESULT 7
US-09-792-793A-85
Sequence 85, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 85
LENGTH: 254
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Methionine-Saporin fusion
US-09-792-793A-85

Query Match 21.2% Score 342; DB 9; Length 254;
Best Local Similarity 35.9% Pred. No. 1.1e-23;
Matches: 94; Conservative 51; Mismatches 97; Indels 20; Gaps 9;
QY 25 INTITDAGNATINKYATFMSLRNOAKDPKLCYGPW-LPDNSTPKYLLVKJGAGNL 83
DB 2 VTSITLDVNPAGQYSSFDKIRNNVKDPNLYGCTDAVIGPPSKKFLRNFOSR- 60
QY 84 KTITMLRRNNLYVMGYSDPPFNGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSN 142
DB 61 GTVSLGKRDNLVYVAYLAMDTNVRNRYFRSEITSAST-----ALFPEATANOKALE 116
QY 143 YNSLYPTMEKAEV-----NSRNQVQIGTIOILSSDICKISCVDSFPVKTAEFFLLVIAQW 198
DB 117 YTEDYOSIEKNAQITOGDOSRKELGIDLLSTSMCAVN-KKARVVKDEARFLLAIUMT 175
QY 199 SEARKEYTENQVTFNRAFYDPKVINIEKWKISAEIH-NAKNGALPKPLFLVIAK 257
DB 176 AEARERYIQNLVIRKPNFNSKNVIOFVNNKKISTAIYGDAGKNGVFNKIDYDFG 235
QY 258 GTXKIVLRVDEINROVALLKYV 279
DB 236 -----VRQVKDL--QMGLLYL 250

RESULT 8
US-09-792-793A-15
Sequence 35, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15

06/02/2003

105

QY 241 NAKNGALPKPLRLVDAGTKWIVLRVDEINRDVALLKYVNGTCOTTQYQNAFMSQVILSTY 300
DB 241 NAKNGALPKPLRLVDAGTKWIVLRVDEINRDVALLKYVNGTCOTTQYQNAFMSQVILSTY 300
QY 301 YNYMSNLGDLFEFG 314
DB 301 YNYMSNLGDLFEFG 314

RESULT 2
US-09-978-274A-4
: Sequence 4, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978, 274A
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 263
: TYPE: PRT
: ORGANISM: Phytolacca americana
US-09-978-274A-4

Query Match 83.6%; Score 1352; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 6e-117;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 INTITFDAGNATINKYATFMSLRNOAKDPKLCYGPIMPLDPTNSTPKYLLVKLOGANLK 84
DB 2 INTITFDAGNATINKYATFMSLRNOAKDPKLCYGPIMPLDPTNSTPKYLLVKLOGANLK 61
QY 85 TITLMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 144
DB 62 TITLMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 121
QY 145 SLYPTMEKKAENVSRNOVOLGQILSSDQIGKISGVDSFPVKTEAFFLLVAIQMVSEAAAF 204
DB 122 SLYPTMEKKAENVSRNOVOLGQILSSDQIGKISGVDSFPVKTEAFFLLVAIQMVSEAAAF 181
QY 205 KYIENOVKTNFRAPYDPKPKVINLEEKWKXISEATHNAKNGALPKPLRLVDAGTKWIVL 264
DB 182 KYIENOVKTNFRAPYDPKPKVINLEEKWKXISEATHNAKNGALPKPLRLVDAGTKWIVL 241
QY 265 RVDEINRDVALLKYVNGTCOTT 286
DB 242 RVDEINRDVALLKYVNGTCOTT 263

RESULT 3
US-09-978-274A-6
: Sequence 6, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978, 274A
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14

: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6
: LENGTH: 154
: TYPE: PRT
: ORGANISM: Phytolacca americana
US-09-978-274A-6

Query Match 48.7%; Score 788; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.5e-65;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 INTITFDAGNATINKYATFMSLRNOAKDPKLCYGPIMPLDPTNSTPKYLLVKLOGANLK 84
DB 2 INTITFDAGNATINKYATFMSLRNOAKDPKLCYGPIMPLDPTNSTPKYLLVKLOGANLK 61
QY 85 TITLMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 144
DB 62 TITLMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 121
QY 145 SLYPTMEKKAENVSRNOVOLGQILSSDQIGKIS 177
DB 122 SLYPTMEKKAENVSRNOVOLGQILSSDQIGKIS 154

RESULT 4
US-09-978-274A-8
: Sequence 8, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978, 274A
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 8
: LENGTH: 110
: TYPE: PRT
: ORGANISM: Phytolacca americana
US-09-978-274A-8

Query Match 34.9%; Score 564; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.1e-44;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 178 GVDSPVKTEAFFLLVAIQMVSEAAAFKYIENOVKTNFRAPYDPKPKVINLEEKWKXISE 217
DB 2 GVDSPVKTEAFFLLVAIQMVSEAAAFKYIENOVKTNFRAPYDPKPKVINLEEKWKXISE 61
QY 238 AHNKNGALPKPLRLVDAGTKWIVLRVDEINRDVALLKYVNGTCOTT 286
DB 62 AHNKNGALPKPLRLVDAGTKWIVLRVDEINRDVALLKYVNGTCOTT 110

RESULT 5
US-09-792-793A-73
: Sequence 73, Application US/09792793A
: Patent No. US2002016370A1
: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Corbins, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
: FILE REFERENCE: 2502-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22

09978274

SRNT

Printed 11/17/2004

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CM protein - protein search, using sw model

Run on: May 28, 2003, 09:58:20 ; Search time 58 seconds
(without alignments)
536,900 Million cell updates/sec

Title: US-09-978-274A-2

Perfect score: 1617

Sequence: 1 MKVMLVVVVTLIAWLIAPT.....VILSTYNYMNLGOLFEGF 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published_Applications_AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1617	100.0	314	10	US-09-978-274A-2
2	1352	83.6	263	10	US-09-978-274A-4
3	788	48.7	154	10	US-09-978-274A-6
4	564	34.9	110	10	US-09-978-274A-8
5	346	21.4	332	9	US-09-792-793A-73
6	343.5	21.2	330	9	US-09-792-793A-82
7	342	21.2	254	9	US-09-792-793A-85
8	342	21.2	275	9	US-09-792-793A-35
9	342	21.2	327	9	US-09-792-793A-79
10	342	21.2	332	9	US-09-792-793A-76
11	325	20.1	293	10	US-09-765-527-259
12	325	20.1	309	10	US-09-765-527-253
13	325	20.1	332	10	US-09-765-527-251
14	312	19.3	251	10	US-09-765-527-247
15	261	16.1	250	9	US-09-792-793A-36
16	240	14.8	240	9	US-09-792-793A-39
17	225	13.9	247	9	US-09-792-793A-34
18	204	12.6	252	10	US-09-347-064-2
19	204	12.6	252	10	US-09-347-064-8

20	130.5	8.1	315	10	US-09-334-477-2	Sequence 2, Appl
21	130.5	8.1	323	10	US-09-334-477-21	Sequence 21, Appl
22	130	8.0	323	9	US-09-792-793A-80	Sequence 80, Appl
23	130	8.0	325	9	US-09-792-793A-81	Sequence 81, Appl
24	125.5	7.8	325	9	US-09-792-793A-74	Sequence 74, Appl
25	125.5	7.8	327	9	US-09-792-793A-75	Sequence 75, Appl
26	124	7.7	325	9	US-09-792-793A-71	Sequence 71, Appl
27	124	7.7	327	9	US-09-792-793A-72	Sequence 72, Appl
28	123	7.6	326	10	US-09-334-477-37	Sequence 37, Appl
29	123	7.6	650	10	US-09-334-477-47	Sequence 47, Appl
30	123	7.6	708	10	US-09-334-477-33	Sequence 33, Appl
31	122	7.5	320	9	US-09-792-793A-77	Sequence 77, Appl
32	122	7.5	322	9	US-09-792-793A-78	Sequence 78, Appl
33	121	7.5	319	9	US-09-792-793A-38	Sequence 38, Appl
34	121	7.5	319	9	US-09-870-759-28	Sequence 28, Appl
35	120	7.4	247	9	US-09-792-793A-83	Sequence 83, Appl
36	120	7.4	249	9	US-09-792-793A-84	Sequence 84, Appl
37	120	7.4	293	9	US-09-792-793A-37	Sequence 37, Appl
38	119.5	7.4	694	10	US-09-334-477-49	Sequence 49, Appl
39	112.5	7.0	318	10	US-09-334-477-6	Sequence 6, Appl
40	112.5	7.0	326	10	US-09-334-477-25	Sequence 25, Appl
41	111	6.9	329	10	US-09-334-477-39	Sequence 39, Appl
42	111	6.9	711	10	US-09-334-477-35	Sequence 35, Appl
43	95.5	5.9	1447	10	US-09-797-097-2	Sequence 2, Appl
44	93	5.8	1974	9	US-09-895-913A-12	Sequence 12, Appl
45	89.5	5.5	930	10	US-09-815-242-10779	Sequence 10779, A

ALIGNMENTS

RESULT 1

US-09-978-274A-2
: Sequence 2, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978,274A
: PRIOR FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 314
: TYPE: PKT
: ORGANISM: Phytolacca americana
US-09-978-274A-2

Query Match	100.0%	Score 1617;	DB 10;	Length 314;
Best Local Similarity	100.0%;	Pred. No. 2.6e+141;		
Matches: 314;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Oy	1	MKVMLVVVVVTLIAWLI.AAPTSTCAINTITFDAGNATINKYATFMESLRNOAKDPKIKYCG	60	
Db	1	MKVMLVVVVVTLIAWLI.AAPTSTCAINTITFDAGNATINKYATFMESLRNOAKDPKIKYCG	60	
Oy	61	TPMLPDTNSTPKYILVKLOGANIKTITLIMLRNNLYVNCYSDDPFGNCKRYIIFNDITST	120	
Db	61	TPMLPDTNSTPKYILVKLOGANIKTITLIMLRNNLYVNCYSDDPFGNCKRYIIFNDITST	120	
Oy	121	ERTDVENTLCSSSSSKVAMSYNNSLYPTMEKKAEVNSRNQVGLGQITLSSDICKISVD	180	
Db	121	ERTDVENTLCSSSSSKVAMSYNNSLYPTMEKKAEVNSRNQVGLGQITLSSDICKISVD	180	
Oy	181	SFPVKTEAFFLLVATQWSEAKPKYIENOVKTNPKNFYPOPKVINLEEKWKISVAII	240	
Db	181	SFPVKTEAFFLLVATQWSEAKPKYIENOVKTNPKNFYPOPKVINLEEKWKISVAII	240	

240 RVDEIKPDVGLLNYVNGTCQAT 261

RESULT 15

0009-610-838-9

Sequence 9, Application US/09610838

Patent No. 6376217

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Sudhika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Heid & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/610,838

FILING DATE: 06-JUL-2000

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/136,389

FILING DATE: 18-AUG-1998

APPLICATION NUMBER: 08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70-P4

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

0009-610-838-9

Query Match

Score 1096.5; DB 4: Length 261;

Best Local Similarity

82.8%; Pred. No. 1.5e-101;

Matches 217; Conservative

14; Mismatches 30; Indels 1; Caps 1;

25 INTTFDAGNATINKYATPMESLRNQAQPKLCYGIPLPDNTNTPKYLVLKQGANLK 84

1 INTTFDAGNATINKYATPMESLRNQAQPKLCYGIPLPDNTNTPKYLVLKQGANLK 60

QY 85 TITLMLRRNNLYVMGYSDPENGKCRHYHFNIDITSTERTDVENTLSSSSSRVAMSINTN 144
|||||
DB 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKGTEYSOVENTLCPSSNPVAKPYN 119
|||||
QY 145 SLYPTMFKKAEVNSRNVOLGIGIILSSDICKISGVDSFPVKTEAFFILVAIONVSAARF 204
|||||
DB 120 GLYPTLEKKAGVTSRNEVOLGIGIILSSDICKISGVDSFPVKTEAFFILVAIONVSAARF 179
|||||
QY 205 KYTENOVKTNFNEAFYDPKVINLEKKWCKISFATHNKNKNGALPKPLELVDAKGTWKIVL 264
|||||
DB 180 KYTENOVKTNFNKFDFNDKVLPLEENWCKISFATHNKNKNGALPKPLELVDAKGTWKIVL 239
|||||
QY 265 RVDEINRQVALIKYVNGTCQAT 286
|||||
DB 240 RVDEIKPDVGLLNYVNGTCQAT 261
|||||

Search completed: May 28, 2003, 09:59:41
Job time : 31 secs

SRNT

0009-610-838-9

Printed

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530,
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 110220US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-839-765-9

TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-9

Query Match 67.8% Score 1096.5; DB 4; Length 261;
Best Local Similarity 82.8% Pred. No. 1.5e-101;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
QY 25 INTITFDAGNATINKYATNESLRNQAOKPKLCKYGPMLPDTNSTPKYLLVKLQGANLK 84
DB 1 INTITFDAGNATINKYATNESLRNQAOKPKLCKYGPMLPDTNSTPKYLLVKLQGANLK 60
QY 85 TITLMLRRNLNLYVMGYSDPDYD-NKCRYHIFNDIKGTEYSDVENTLCPSSNPRVAKPINYN 144
DB 61 TITLMLRRNLNLYVMGYSDPDYD-NKCRYHIFNDIKGTEYSDVENTLCPSSNPRVAKPINYN 119
QY 145 SLYPTMEKKAENSVNRNOVLGQILSSDICKISGVDSFPVKTEAFELLVAIQVSSAARF 204
DB 120 GLYPTLEKKAGVTSRNEVQLGQILSSDICKISGVDSFPVKTEAFELLVAIQVSSAARF 179
QY 205 KYIENOVKTNFNRAFPDPKVINLEEKWKIKISFAIHNAKNGALPKPLGLVDAGTKWIVL 264
DB 180 KYIENOVKTNFNRAFPDPKVINLEEKWKIKISFAIHNAKNGALPKPLGLVDAGTKWIVL 239
QY 265 RVDEINRDVALKYVNGTQOTT 286
DB 240 RVDEIKPDVGLLNYVNGTQOAT 261

Query Match 67.8% Score 1096.5; DB 4; Length 261;
Best Local Similarity 82.8% Pred. No. 1.5e-101;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
QY 25 INTITFDAGNATINKYATNESLRNQAOKPKLCKYGPMLPDTNSTPKYLLVKLQGANLK 84
DB 1 INTITFDAGNATINKYATNESLRNQAOKPKLCKYGPMLPDTNSTPKYLLVKLQGANLK 60
QY 85 TITLMLRRNLNLYVMGYSDPDYD-NKCRYHIFNDIKGTEYSDVENTLCPSSNPRVAKPINYN 144
DB 61 TITLMLRRNLNLYVMGYSDPDYD-NKCRYHIFNDIKGTEYSDVENTLCPSSNPRVAKPINYN 119
QY 145 SLYPTMEKKAENSVNRNOVLGQILSSDICKISGVDSFPVKTEAFELLVAIQVSSAARF 204
DB 120 GLYPTLEKKAGVTSRNEVQLGQILSSDICKISGVDSFPVKTEAFELLVAIQVSSAARF 179
QY 205 KYIENOVKTNFNRAFPDPKVINLEEKWKIKISFAIHNAKNGALPKPLGLVDAGTKWIVL 264
DB 180 KYIENOVKTNFNRAFPDPKVINLEEKWKIKISFAIHNAKNGALPKPLGLVDAGTKWIVL 239
QY 265 RVDEINRDVALKYVNGTQOTT 286
DB 240 RVDEIKPDVGLLNYVNGTQOAT 261

Sequence 9, Application US/09136389
Sequence No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-9

Query Match 67.8%; Score 1096.5; DB 1; Length 261;
Best Local Similarity 82.8%; Pred. No. 1.5e-101;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
Y 25 INITFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKLOGANLK 84
b 1 INITFDAGNATINKYATFMSLRNEAKDPSLKCYGIPMLPNTNSTIKYLLVKLOGASLK 60
Y 85 TITLMLRRNLNLYVMGYSDFPENGKCRYHFNIDITSTERTDVENTICSSSSSRVAMSYN 144
b 61 TITLMLRRNLNLYVMGYSDFPENGKCRYHFNIDITSTERTDVENTICSSSSSRVAKPNTN 119
Y 145 SLYPTMEKKAENSRNOVGLGIGTLLSSDICKISGVDSFPVKTEAFELLVAIQWSEAAAF 204
b 120 GLYPTLEKKAGVTSRNEVGLGIGTLLSSDICKISGVDSFPVKTEAFELLVAIQWSEAAAF 179
Y 205 KYIENQVKTNFNRAPYDPKVINLEEKWKISAEAHNANGALPKPPLVLDVADAGTKWIVL 264
b 180 KYIENQVKTNFNRDFSPNDKVLDELFNWCKISTAHNSKNGALPKPPLVLDVADAGTKWIVL 239
Y 265 RVDEINRROVALLKYVNGTCQT 286
b 240 RVDEIKPDVGLLNYNGTCQT 261

RESULT 12
US-08-646-360-9
Sequence 9, Application US/08646360
Patent No. 5937491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/054,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-9
Query Match 67.8%; Score 1096.5; DB 2; Length 261;
Best Local Similarity 82.8%; Pred. No. 1.5e-101;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
Y 25 INITFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKLOGANLK 84
b 1 INITFDAGNATINKYATFMSLRNEAKDPSLKCYGIPMLPNTNSTIKYLLVKLOGASLK 60
Y 85 TITLMLRRNLNLYVMGYSDFPENGKCRYHFNIDITSTERTDVENTICSSSSSRVAMSYN 144
b 61 TITLMLRRNLNLYVMGYSDFPENGKCRYHFNIDITSTERTDVENTICSSSSSRVAKPNTN 119
Y 145 SLYPTMEKKAENSRNOVGLGIGTLLSSDICKISGVDSFPVKTEAFELLVAIQWSEAAAF 204
b 120 GLYPTLEKKAGVTSRNEVGLGIGTLLSSDICKISGVDSFPVKTEAFELLVAIQWSEAAAF 179
Y 205 KYIENQVKTNFNRAPYDPKVINLEEKWKISAEAHNANGALPKPPLVLDVADAGTKWIVL 264
b 180 KYIENQVKTNFNRDFSPNDKVLDELFNWCKISTAHNSKNGALPKPPLVLDVADAGTKWIVL 239
Y 265 RVDEINRROVALLKYVNGTCQT 286
b 240 RVDEIKPDVGLLNYNGTCQT 261

RESULT 13
US-08-839-765-9
Sequence 9, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:

Best Local Similarity 82.8%; Pred. No. 1.5e-101;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
25 INTITDAGNATINKYATFMSLRNKAQPKLKYCIGIPMLPDTNSTPKYLKLVKLGANLK 84
1 INTITDAGNATINKYATFMSLRNKAQPKLKYCIGIPMLPDTNSTPKYLKLVKLGASLK 60
85 TITMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLCCSSSSSRVAMSYN 144
61 TITMLRRNNLYVMGYSDPYD-NKCRYHIFNDIKGTESDVENTLCPSSNPRVAKPINYN 119
145 SLYPTMEKKAENSRNQVQLGIGIILSSDICKISGVDSFPVKTEAFELLVAIQWSEARF 204
120 GLYPTLEKAGVTSRNEVQLGIGIILSSDICKISGVDSFPVKTEKIEAKFLLVAIQWSEARF 179
205 KYTENOVKTNFNRFPDVKVINLEEKWKISIAHNKNGALPKPLKLNADGTTKIVL 264
180 KYTENOVKTNFNRDPSNDKVLDEENWGKISTAIHNSKNGALPKPLKLNADGTTKIVL 239
265 RVDEINRDVALLKYVNGTCOTT 286
240 RVDEIKPDVGLLYVNGTCOAT 261

RESULT 10
US-08-488-113B-9
Sequence 9, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155

TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-9
Query Match 67.8%; Score 1096.5; DB 1: Length 261;
Best Local Similarity 82.8%; Pred. No. 1.5e-101;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
25 INTITDAGNATINKYATFMSLRNKAQPKLKYCIGIPMLPDTNSTPKYLKLVKLGANLK 84
1 INTITDAGNATINKYATFMSLRNKAQPKLKYCIGIPMLPDTNSTPKYLKLVKLGASLK 60
85 TITMLRRNNLYVMGYSDPFNGNCKRYHIFNDITSTERTDVENTLCCSSSSSRVAMSYN 144
61 TITMLRRNNLYVMGYSDPYD-NKCRYHIFNDIKGTESDVENTLCPSSNPRVAKPINYN 119
145 SLYPTMEKKAENSRNQVQLGIGIILSSDICKISGVDSFPVKTEAFELLVAIQWSEARF 204
120 GLYPTLEKAGVTSRNEVQLGIGIILSSDICKISGVDSFPVKTEKIEAKFLLVAIQWSEARF 179
205 KYTENOVKTNFNRFPDVKVINLEEKWKISIAHNKNGALPKPLKLNADGTTKIVL 264
180 KYTENOVKTNFNRDPSNDKVLDEENWGKISTAIHNSKNGALPKPLKLNADGTTKIVL 239
265 RVDEINRDVALLKYVNGTCOTT 286
240 RVDEIKPDVGLLYVNGTCOAT 261

RESULT 11
US-08-477-484B-9
Sequence 9, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

Query Match 75.9% Score 1227.5 DB 4: Length 313:
Best Local Similarity 75.6% Pred. No. 1.6e-114: Mismatches 41: Indels 3: Gaps 2:
Matches 238: Conservative 33: Mismatches 41: Indels 3: Gaps 2:

1 MKVMLVVVTLAWLIZAPTSCAINTITFDAGNATINKYATFMSLRNOAKOPKLCYCG 60
1 MKSMLVVVTISI--WLIAPTSTWAVNTIYVVGSTISKYATFMRNLNRNEAKDPSLCYCG 58

61 IMLPDTNSTPKYLLVKKLOGANIKTTITMLRRNNLVYMGYSDFPFGNKNCRHYHFNIDTST 120
59 IMLPNTNPNKHLVVELOGSNKKTTITMLRRNNLVYMGYSDFPFGNKNCRHYHFNIDTST 118

121 ERTDVENTICSSSSSRVAMSIYNSLYPTMEKKAENSRNOVOLGQIILSSDGIKISGVD 180
119 ERQDVEITLCPNANSRVSKNIINFSRYPTLESKAGVKSQVOLGQIILSSDGIKISGVD 178

181 SPVKTAEFFLLVAIQVSEAAARFKYIENQVKTNFRAFYDPKVINLEEKMGKISEATH 240
179 SITEKTEAEFFLLVAIQVSEAAARFKYIENQVKTNFRAFYDPKVINLEEKMGKISEATH 238

241 NAKGNALPKPLELDVAKGTWIVLRVDEINROVALLKYVNGTCQTTY-ONAMFSQVLIIST 299
239 DAKGNVLPKPLELDVAGAKWIVLRVDEIKPDVALLNYYVGGSCQTTYONAMFPOLIMST 298

300 YNYMSNLGLDFEGF 314
299 YNYMVNGLDFEGF 313

RESULT 8
US-08-378-761A-79
Sequence 79, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-79

Query Match 67.8% Score 1096.5 DB 1: Length 261:
Best Local Similarity 82.8% Pred. No. 1.5e-101:
Matches 217: Conservative 14: Mismatches 30: Indels 1: Gaps 1:

25 INTITFDAGNATINKYATFMSLRNOAKDPKLCYCGIPLMDPTNSTPKYLLVKKLOGANIK 84
1 INTITFDAGNATINKYATFMSLRNEAKDPSLCYCGIPLMDPTNSTIKYLLVKKLOGASLK 60

85 TITMLRRNNLVYMGYSDFPFGNKNCRHYHFNIDTSTERTDVENTICSSSSSRVAMSIYNY 144
61 TITMLRRNNLVYMGYSDFPFGNKNCRHYHFNIDTSTERTDVENTICSSSNPRVAKIPINY 119

145 SLYPTMEKKAENSRNOVOLGQIILSSDGIKISGVDSPFKTEAFELLVAIQVSEAAARF 204
120 GLYPTLEKKAQVTSRNEVOLGQIILSSDGIKISGQSFTKEAKELLVAIQVSEAAARF 179

205 KYIENQVKTNFRAFYDPKVINLEEKMGKLSFATHNKNAGALPKPLIPLVDKGTWKWIVL 264
180 KYIENQVKTNFRAFYDPKVINLEEKMGKLSFATHNKNAGALPKPLIPLVDKGTWKWIVL 239

265 RVDEINROVALLKYVNGTCQTTY 286
240 RVDEJKPDVGLNLYVNGTCQAT 261

RESULT 9
US-08-485-286-79
Sequence 79, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-79

Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;

1 MKVMLVVVVTLIAWLIAPTSTCAINTITFDAGNATINKYATFMSLRNQAKDPKLCYG 60
1 MKSMLVVTISI--WLLAPTSTWAVNTIYVGVSTTISKYATFLNDRNEAKDPSLKCYG 58
61 IMLPDTNSTPKYLVKLOGANKTITLMLRNNLYVMGYSDPFNGKCRHYHENDITST 120
59 IMLPNTNPKYVLELQGSNKKTTITLMLRNNLYVMGYSDPFETNCKRYHENDISCT 118
121 BRTDVENTLCCSSSSSRVAMSINYSIYPTMEKKAENSRNQVQLGIGIQLSSDIGKISGV 180
119 ERQDVETTLCPNANRVRKNNFDSRYPTLESKAGVRSQVQLGIGIQLSSDIGKISGV 178
181 SPVKTEAFFLLVAIOMYSEARFKYIENOVKTENFRFYPPKVINLEEKWKI SEATH 240
179 SFTKTEAEFLVLAJOMYSEARFKYIENOVKTENFRFNPNKVLNQTWCKISTAIH 238
241 NAKNGALPKPLEVDAGKTKWIVLRVDEINRDVALLKYVNGTCOTTY-ONAMFSQVIIST 299
239 DAKNGVLPKPLEVDASGAKWIVLRVDEIKPDVALLNYVGGSCOTTYNQAMFPOLINST 298
300 YNYMNLGDLFEFG 314
299 YNYMNLGDLFEFG 313

RESULT 6
US-08-501-253A-2
Sequence 2, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
TITLE OF INVENTION: Bioregulatory Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-501-253A-2

Query Match 76.2%; Score 1232.5; DB 4; Length 313;
Identical Similarity 75.6%; Pred. No. 5e-115;
Matches 238; Conservative 34; Mismatches 40; Indels 3; Gaps 2;

1 MKVMLVVVVTLIAWLIAPTSTCAINTITFDAGNATINKYATFMSLRNQAKDPKLCYG 60

099/8274

06/02/2003

112

SRNT

Printed 11/17/2004

1 MKSMLVVTISI--WLLAPTSTWAVNTIYNVGGSTTISKYATFLNDRNEAKDPSLKCYG 58
61 IMLPDTNSTPKYLVKLGANLKITLMLRRNNLVYMGYSOPFNGNCKRYHIFNDITST 120
59 IMLPNTNPKYLVVLOGSNKKTTITLMLRRNNLVYMGYSOPFETNCKRYHIFNDISGT 118
121 ERTDVENTLCSSSSRVAMSINYSLYPTMEKKAENSHNOVOLGQILSSDTGKISGVD 180
119 ERDQVETTLCPNANSRVSKNINFDSPRYPTLESKAGVKSRSVOLGQILDSNIGKISGVM 178
181 SFVKTEAEFLVAIQMSEAAAREFYIENQVKTENRAFYPDPKVINLEEKWKISEALH 240
179 SPTEKTEAEFLVAIQMSEAAAREFYIENQVKTENRAFNPKNPKVLNLOETWCKISTAH 238
241 NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCQTTY-ONAMESQVIST 299
239 DAKNGVLPKPLELDVDAKGTWIVLRVDEIKPDVALLNYVGGSCQTTYNONAMFPQLIMST 298
300 YNYMSNLGDLFEGF 314
299 YNYMVNUGDLFEGF 313

RESULT 4

JS-09-005-273-2
Sequence 2, Application US/09005273
Patent No. 613/030
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-005-273-2

Query Match 76.4% Score 1235.5; DB 4; Length 313;
Best Local Similarity 75.9%; Pred. No. 2.5e-115;
Matches 239; Conservative 33; Mismatches 40; Indels 2;
Gaps 2;
QY 1 MKMVLVVVTLIAWLIAPTSTCAINTITFDAGNATINKYATFENESLRNOAKDPSLKCYG 60
DB 1 MKSMLVVTISI--WLLAPTSTWAVNTIYNVGGSTTISKYATFLNDRNEAKDPSLKCYG 58
QY 61 IMLPDTNSTPKYLVKLGANLKITLMLRRNNLVYMGYSOPFNGNCKRYHIFNDITST 120
DB 59 IMLPNTNPKYLVVLOGSNKKTTITLMLRRNNLVYMGYSOPFETNCKRYHIFNDISGT 118
QY 121 ERTDVENTLCSSSSRVAMSINYSLYPTMEKKAENSHNOVOLGQILSSDTGKISGVD 180
DB 119 ERDQVETTLCPNANSRVSKNINFDSPRYPTLESKAGVKSRSVOLGQILDSNIGKISGVM 178
QY 181 SFVKTEAEFLVAIQMSEAAAREFYIENQVKTENRAFYPDPKVINLEEKWKISEALH 240
DB 179 SPTEKTEAEFLVAIQMSEAAAREFYIENQVKTENRAFNPKNPKVLNLOETWCKISTAH 238
QY 241 NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCQTTY-ONAMESQVIST 299
DB 239 DAKNGVLPKPLELDVDAKGTWIVLRVDEIKPDVALLNYVGGSCQTTYNONAMFPQLIMST 298
QY 300 YNYMSNLGDLFEGF 314
DB 299 YNYMVNUGDLFEGF 313

RESULT 5

PCT-US96-11546-2
Sequence 2, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
MUTANTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-11546-2

Query Match 76.4% Score 1235.5; DB 5; Length 313;
Best Local Similarity 75.9%; Pred. No. 2.5e-115;

TISSUE TYPE: Leaf
898-373-858-2

Query Match 76.4% Score 1235.5; DB 1: Length 313;
Best Local Similarity 75.9% Pred. No. 2.5e-115;
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;

```
Qy 1 MKVMLVVVTLIAWLIAPTSTCAINTITFDAGNATINKYATFESLRNOAKOPKLCYCG 60
Db 1 MKSMLVVTISI--WLILAPTSTWAVNTIYNVGSSTTISKYATFELNDRNEAKOPSLKCYG 58
Qy 61 IPMLPDTNSTPKYLLVVKLOGANLKTITLMLRRNNLYVMGYSDFPENGKCRHYHNDITST 120
Db 59 IPMLPNTNTNPKYVLVLEQGSNKKITITLMLRRNNLYVMGYSDFPENGKCRHYHNDISGT 118
Qy 121 ERTDVENTLCSSSSSRVAMSNLYPTMEKKAEVNRNOVQLGQILSSDICKISGVD 180
Db 119 ERQDVEITLCPNANRSVSKNINFDOSRYPTLESKAGVKSRSQVQLGQILDSNICKISGVM 178
Qy 181 SFPVKTEAFFLLVAIQNVSEAAAREKYIENQVKTNFNRAFYPDPKVINLEEKWKISGAII 240
Db 179 SFTKTEAEFLVAIQNVSEAAAREKYIENQVKTNFNRAFNPKNLQETWKGKISTAIH 238
Qy 241 NAKNGALPKLELVDAKCTKWILRVDEINRDVALLKYVNGTCOTTY--QNAFMSQVITST 299
Db 239 DAKNGVLPKPLELVDAKAKWILRVDELKPDVALLNLYVGGSCOTTYNONAMFPQLIMST 298
Qy 300 YNNYMSNLGDLPEGF 314
Db 299 YNNYMNGLDLPEGF 313
```

RESULT 2

US-08-500-611-2
Sequence 2, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 11-JUL-1995
APPLICATION NUMBER: US/08/500.611
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-500-611-2

Printed 11/17/2004

Query Match 76.4% Score 1235.5; DB 1: Length 313;
Best Local Similarity 75.9% Pred. No. 2.5e-115;
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;

```
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;
Qy 1 MKVMLVVVTLIAWLIAPTSTCAINTITFDAGNATINKYATFESLRNOAKOPKLCYCG 60
Db 1 MKSMLVVTISI--WLILAPTSTWAVNTIYNVGSSTTISKYATFELNDRNEAKOPSLKCYG 58
Qy 61 IPMLPDTNSTPKYLLVVKLOGANLKTITLMLRRNNLYVMGYSDFPENGKCRHYHNDITST 120
Db 59 IPMLPNTNTNPKYVLVLEQGSNKKITITLMLRRNNLYVMGYSDFPENGKCRHYHNDISGT 118
Qy 121 ERTDVENTLCSSSSSRVAMSNLYPTMEKKAEVNRNOVQLGQILSSDICKISGVD 180
Db 119 ERQDVEITLCPNANRSVSKNINFDOSRYPTLESKAGVKSRSQVQLGQILDSNICKISGVM 178
Qy 181 SFPVKTEAFFLLVAIQNVSEAAAREKYIENQVKTNFNRAFYPDPKVINLEEKWKISGAII 240
Db 179 SFTKTEAEFLVAIQNVSEAAAREKYIENQVKTNFNRAFNPKNLQETWKGKISTAIH 238
Qy 241 NAKNGALPKLELVDAKCTKWILRVDEINRDVALLKYVNGTCOTTY--QNAFMSQVITST 299
Db 239 DAKNGVLPKPLELVDAKAKWILRVDELKPDVALLNLYVGGSCOTTYNONAMFPQLIMST 298
Qy 300 YNNYMSNLGDLPEGF 314
Db 299 YNNYMNGLDLPEGF 313
```

RESULT 3

US-08-500-694-2
Sequence 2, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 11-JUL-1995
APPLICATION NUMBER: US/08/500.694
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-500-694-2

Query Match

Query Match 76.4% Score 1235.5; DB 2: Length 313;
Best Local Similarity 75.9% Pred. No. 2.5e-115;
Matches 239; Conservative 33; Mismatches 40; Indels 3; Gaps 2;

RESULT 15
AA81496/c
ID AAX81496 standard: DNA; 1956 BP.

XX
AC AAX81496;

XX
DT 24-AUG-1999 (first entry)

XX
DE DNA sequence of cry3Bb.11058 gene.

XX
DE Cry3Bb; mutant; insecticidal activity; insecticidal specificity;
KW coleoptera; southern corn rootworm; western corn root worm;
KW Diabrotica undecimpunctata howardi Barber; transgenic plant;
KW Diabrotica virgifera virgifera LeConte; insecticide resistance; ss.

XX
OS Synthetic.

OS Bacillus thuringiensis.

XX
PN W09931248-A1.

XX
PD 24-JUN-1999.

XX
PF 17-DEC-1998; 98WO-US26852.

XX
PR 18-DEC-1997; 97US-0996441.

XX
PR 18-DEC-1997; 97US-0993170.

XX
PR 18-DEC-1997; 97US-0993722.

XX
PR 18-DEC-1997; 97US-0993775.

XX
PA (ECOC-) ECOGEN INC.

PA (MONS) MONSANTO CO.

XX
PI Brussock SM, Bryson JW, English L, Kulesza CA, Malvar TM;

PI Romano C, Slatin SL, Von Tersch MA, Walters FS;

XX
DR WPI; 1999-395184/33.

XX
PT Insecticidal Bacillus thuringiensis proteins

XX
PT Claim 52: Page 426-429; 512pp; English.

XX
PS AAX81468-x81502, AAX81529 and AAX81532 encode new Bacillus thuringiensis
CC Cry3Bb mutant proteins. The specification also describes methods of
CC altering Bacillus thuringiensis Cry3Bb. The B. thuringiensis Cry3Bb
CC polypeptide was modified to have improved insecticidal activity or
CC enhanced insecticidal specificity against a target insect. The
CC modification comprises at least one amino acid substitution, addition,
CC or deletion in the primary sequence of the native or unmodified Cry3Bb
CC polypeptide, wherein the substitution or deletion occurs at a position
CC corresponding to from about amino acids 1-365 of the unmodified
CC polypeptide sequence (AAX81528 and AAX81531 encode the wild type Cry3Bb
CC protein). The polypeptide can be used to kill coleopteran pests,
CC especially by application to the environment. It is especially
CC useful against southern corn rootworm and western corn root worm,
CC (Diabrotica undecimpunctata howardi Barber, and Diabrotica virgifera
CC virgifera LeConte respectively). The mutant cry3Bb polynucleotides
CC can also be used to produce transgenic plants with increased
CC insecticide resistance.

XX
SQ Sequence 1956 BP; 683 A; 315 C; 344 G; 614 T; 0 other;

Query Match 2.1% Score 20; DB 20; Length 1956;

Best Local Similarity 100.0%; Pred. No. 8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 ACTTCAACTTGTGCCATAAA 77

DB 344 ACTTCAACTTGTGCCATAAA 325

Search completed: June 2, 2003, 04:22:00
Job time : 292 secs

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 844 ACTGTCAGACAACTTACCATAA 865
 Db 1974 ACTGTCAGACAACTTACCATAA 1995

RESULT 13

AAX81493/C
 ID AAX81493 standard: DNA: 1956 BP.

XX AC AAX81493:

XX DT 24-AUG-1999 (first entry)

XX DE DNA sequence of cry3Bb.11048 gene.

XX KW Cry3Bb: mutant; insecticidal activity; insecticidal specificity;
 XX KW coleoptera; southern corn rootworm; western corn root worm;
 XX KW Diabrotica undecimpunctata howardi Barber; transgenic plant;
 XX KW Diabrotica virgifera virgifera LeConte; insecticide resistance; ss.

XX OS Synthetic.

XX OS Bacillus thuringiensis.

XX PN WO9931248-A1.

XX PD 24-JUN-1999.

XX PF 17-DEC-1998: 98MO-US26852.

XX PR 18-DEC-1997: 97US-0996441.

XX PR 18-DEC-1997: 97US-0993170.

XX PR 18-DEC-1997: 97US-0993722.

XX PR 18-DEC-1997: 97US-0993775.

XX PA (ECOG-) ECOGEN INC.

XX PA (MONS) MONSANTO CO.

XX PI Brussock SM, Bryson JW, English L, Kulesza CA, Malvar TM;

XX P1 Romano C, Slatin SL, Von Tersch MA, Walters FS;

XX DR WPI: 1999-395184/33.

XX PT Insecticidal Bacillus thuringiensis proteins

XX PS Claim 52: Page 409-412: 512pp: English.

XX CC AAX81468-X81502, AAX81529 and AAX81532 encode new Bacillus thuringiensis
 XX CC Cry3Bb mutant proteins. The specification also describes methods of
 XX CC altering Bacillus thuringiensis Cry3Bb. The B. thuringiensis Cry3Bb
 XX CC polypeptide was modified to have improved insecticidal activity or
 XX CC enhanced insecticidal specificity against a target insect. The
 XX CC modification comprises at least one amino acid substitution, addition,
 XX CC or deletion in the primary sequence of the native or unmodified Cry3Bb
 XX CC polypeptide, wherein the substitution or deletion occurs at a position
 XX CC corresponding to from about amino acids 1-365 of the unmodified
 XX CC polypeptide sequence (AAX81528 and AAX81531 encode the wild type Cry3Bb
 XX CC protein). The polypeptide can be used to kill coleopteran pests,
 XX CC especially by application to the environment. It is especially
 XX CC useful against southern corn rootworm and western corn root worm,
 XX CC (Diabrotica undecimpunctata howardi Barber, and Diabrotica virgifera
 XX CC virgifera LeConte respectively). The mutant cry3Bb polynucleotides
 XX CC can also be used to produce transgenic plants with increased
 XX CC insecticide resistance.

XX SQ Sequence 1956 BP: 687 A: 312 C: 346 G: 611 T: 0 other;

Query Match 2.1%; Score 20: DR 20: Length 1956;
 Best Local Similarity 100.0%; Pred. No. 8;

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 58 ACTTCAACTTGTGCCATAAA 77

Db 344 ACTTCAACTTGTGCCATAAA 325

RESULT 14

AAX81495/C

ID AAX81495 standard: DNA: 1956 BP.

XX AC AAX81495:

XX DT 24-AUG-1999 (first entry)

XX DE DNA sequence of cry3Bb.11057 gene.

XX KW Cry3Bb: mutant; insecticidal activity; insecticidal specificity;
 XX KW coleoptera; southern corn rootworm; western corn root worm;
 XX KW Diabrotica undecimpunctata howardi Barber; transgenic plant;
 XX KW Diabrotica virgifera virgifera LeConte; insecticide resistance; ss.

XX OS Synthetic.

XX OS Bacillus thuringiensis.

XX PN WO9931248-A1.

XX PD 24-JUN-1999.

XX PF 17-DEC-1998: 98MO-US26852.

XX PR 18-DEC-1997: 97US-0996441.

XX PR 18-DEC-1997: 97US-0993170.

XX PR 18-DEC-1997: 97US-0993722.

XX PR 18-DEC-1997: 97US-0993775.

XX PA (ECOG-) ECOGEN INC.

XX PA (MONS) MONSANTO CO.

XX PI Brussock SM, Bryson JW, English L, Kulesza CA, Malvar TM;

XX P1 Romano C, Slatin SL, Von Tersch MA, Walters FS;

XX DR WPI: 1999-395184/33.

XX PT Insecticidal Bacillus thuringiensis proteins

XX PS Claim 52: Page 421-423: 512pp: English.

XX CC AAX81468-X81502, AAX81529 and AAX81532 encode new Bacillus thuringiensis
 XX CC Cry3Bb mutant proteins. The specification also describes methods of
 XX CC altering Bacillus thuringiensis Cry3Bb. The B. thuringiensis Cry3Bb
 XX CC polypeptide was modified to have improved insecticidal activity or
 XX CC enhanced insecticidal specificity against a target insect. The
 XX CC modification comprises at least one amino acid substitution, addition,
 XX CC or deletion in the primary sequence of the native or unmodified Cry3Bb
 XX CC polypeptide, wherein the substitution or deletion occurs at a position
 XX CC corresponding to from about amino acids 1-365 of the unmodified
 XX CC polypeptide sequence (AAX81528 and AAX81531 encode the wild type Cry3Bb
 XX CC protein). The polypeptide can be used to kill coleopteran pests,
 XX CC especially by application to the environment. It is especially
 XX CC useful against southern corn rootworm and western corn root worm,
 XX CC (Diabrotica undecimpunctata howardi Barber, and Diabrotica virgifera
 XX CC virgifera LeConte respectively). The mutant cry3Bb polynucleotides
 XX CC can also be used to produce transgenic plants with increased
 XX CC insecticide resistance.

XX SQ Sequence 1956 BP: 684 A: 316 C: 345 G: 611 T: 0 other;

Query Match 2.1%; Score 20: DR 20: Length 1956;
 Best Local Similarity 100.0%; Pred. No. 8;

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 58 ACTTCAACTTGTGCCATAAA 77

Db 344 ACTTCAACTTGTGCCATAAA 325

DR P-PSDB: AAW26773.
 XX
 PT Antiviral proteins of Phytolacca insularis Nakai and their genes
 PT useful in plant antiviral agents and immunoconjugates for the
 PT treatment of AIDS and cancer
 XX
 PS
 XX Claim 2: Page 10-12; 26pp; English.
 CC This polynucleotide comprises the coding region of the Phytolacca
 CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
 CC designated gPIP2 (see AAW26773). The gPIP2 gene was isolated from
 CC leaf genomic DNA by PCR amplification (see AAT99558-59). Another
 CC gene (see AAT99557), encoding a 35.7 kDa protein (see AAW26774)
 CC designated gPIP50, has also been isolated from P. insularis Nakai.
 CC Also claimed are vectors encoding these antiviral proteins and host
 CC cells transformed or transfected with these vectors. E. coli
 CC XL1-Blue MRF⁺ gPIP2 (KCM-10080) host cells are claimed, as is a
 CC process for preparing antiviral protein by cultivating these
 CC cells and purifying the protein from inclusion bodies. The
 CC antiviral proteins and recombinant proteins inhibit protein
 CC synthesis. They can be used as active ingredients of antiviral
 CC agents of plant viruses, and employed in the manufacture of
 CC immunoconjugates for the treatment of AIDS and cancer. The
 CC isolated genes can be used in the breeding of transgenic plants
 CC having viral resistance.
 XX
 SQ Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 other;

Query Match 2.4%; Score 23; DB 19; Length 882;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 289 GTGATGGCGTATTCTGATCCCTT 311
 Db 220 GTGATGGCGTATTCTGATCCCTT 242

RESULT 9
 AAQ64893
 ID AAQ64893 standard; cDNA; 918 BP.
 XX
 AC AAQ64893;
 XX
 DT 17-JAN-1995 (first entry)
 XX
 DE Antiviral protein of Phytolacca insularis Nakai.
 XX
 KW Antiviral; anti-microbial; bacteriocide; ribosome; inhibition;
 KW inactivation; Phytolacca insularis Nakai; ss.
 XX
 OS Phytolacca insularis Nakai.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..918
 FT /*tag= a
 FT /product= Antiviral protein.
 XX
 PN AU648475-B.
 XX
 PD 21-APR-1994.
 XX
 PF 13-OCT-1993; 93AU-0048972.
 XX
 PR 28-AUG-1993; 93KR-0016938.
 XX
 PA (JINR-) JIN RO LTD.
 XX
 PI Hong-seob J, Kwan-ho L, Kyu-whan C, Man-keun K;
 PI Young-ho M;
 XX
 DR WPI: 1994-167848/21.
 DR P-PSDB: AAR54839.
 XX

PT Nucleotide sequence from Phytolacca insularis encoding antiviral
 PT protein - encodes a ribosome inactivating protein which may be
 XX used in antimicrobial compns.
 XX
 PS Claim 1: Page 13; 22pp; English.
 XX
 CC The antiviral protein encoded by this sequence comprises an amino
 CC acid sequence prevalent in ribosome inactivating proteins (See
 CC AAK54840). The protein may be used in anti-microbial compositions.
 XX
 SQ Sequence 918 BP; 294 A; 177 C; 191 G; 256 T; 0 other;

Query Match 2.3%; Score 22; DB 15; Length 918;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 289 CTCATGCGCTATTCTGATCCCT 310
 Db 277 CTCATGCGCTATTCTGATCCCT 298

RESULT 10
 AAT04782
 ID AAT04782 standard; DNA; 918 BP.
 XX
 AC AAT04782;
 XX
 DT 16-MAY-1996 (first entry)
 XX
 DE DNA pJMC201 fragment encoding P. insularis antiviral protein.
 XX
 KW pJMC201: Phytolacca insularis antiviral protein; PIP; Nakai;
 KW primer: amplify: CamV 35S promoter; transgenic plant; potato;
 KW Agrobacterium tumefaciens LBA 4404; plant cell transformation; ss.
 XX
 OS Phytolacca insularis.
 XX
 FH Key Location/Qualifiers
 FT misc_difference 913..915
 FT /*tag= a
 FT /codon= seq:gat, aa:ser
 XX
 PN AU663031-B.
 XX
 PD 21-SEP-1995.
 XX
 PF 04-OCT-1994; 94AU-0074404.
 XX
 PR 21-JUL-1994; 94KR-0017696.
 XX
 PA (JINR-) JIN RO LTD.
 XX
 PI Chul-Hwan K, Hong-Seob J, Kyu-Whan C, Man-Keun K;
 PI Young-Ho M;
 XX
 DR WPI: 1995-358858/47.
 DR P-PSDB: AAR80106.
 XX
 PT Recombinant DNA vector expressing Phytolacca insularis antiviral
 PT protein - for the production of virus resistant transgenic plants
 XX
 PS Example 1: Fig 1; 25pp; English.
 XX
 CC This sequence represents a fragment of a recombinant DNA pJMC201 and
 CC encodes Phytolacca insularis antiviral protein (PIP). This sequence
 CC was isolated from a cDNA library of Phytolacca insularis Nakai using
 CC the primer sequences given in AAT04783-84. The amplified sequence was
 CC used, cloned with the CamV 35S promoter, in the production of a
 CC transgenic plant, pref. potato, using Agrobacterium tumefaciens LBA
 CC 4404 for plant cell transformation.
 XX
 SQ Sequence 918 BP; 294 A; 177 C; 191 G; 256 T; 0 other;

09978274

XX WPI: 2000-062555/05.
DR P-PSDB: AAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
PT viruses and/or fungi .
XX
XX Examples: Page 4-5; 43pp: English.
XX This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
CC catalytically removes a specific adenine residue from a highly conserved
CC stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
CC antiviral protein II (PAP II) protein confers antiviral and or antifungal
CC activities to plants. A DNA molecule encoding a PAP II protein with an
CC intact catalytic active site amino acid residue (E172) is useful for
CC generating transgenic plants. PAP II DNA is useful for generating a
CC transgenic plants (especially cereal crops) through transforming a
CC protoplast or introducing the DNA directly into a plant part prior to
CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
CC activity thus have increased resistance to viruses and/or fungi. Viruses
CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
CC other plants pests including insects, bacteria and nematodes. PAP II DNA
CC is also useful for identifying a PAP II protein having reduced
CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC unlike PAP transgenic plants which are stunted and sterile, PAP II
CC transgenic plants have a normal and fertile phenotype.
XX
XX Sequence 1379 BP: 488 A; 233 C; 269 G; 389 T; 0 other;

Query Match 3.1%; Score 29; DB 21; Length 1379;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 915 TAATCTTGGTGATCTATTGAAGGATCT 943
Db 1136 TAATCTTGGTGATCTATTGAAGGATCT 1164

RESULT 7
AAC87929
JD AAC87929 standard: DNA: 1379 BP.
XX
XX AAC87929;
XX
XX 06-MAR-2001 (first entry)
XX
XX P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
XX
XX Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP;
KW cancer; biotherapeutic; fusion protein; immunocytotoxic; mutant;
KW cytostatic; anti-HIV; human immunodeficiency virus; AIDS; leukaemia;
KW lymphoma; brain tumour; neuroblastoma; soft tissue sarcoma;
KW osteosarcoma; ss.
XX
XX Phytolacca americana.
XX
XX Key Location/Qualifiers
FH CDS 225..1166
FT FT
FT FT
FT FT
XX
XX US6146628-A.
XX
XX 14-NOV-2000.
XX
XX 11-JUL-1995; 9505-0501253.
XX
XX 11-JUL-1995; 9505-0501253.
XX
XX

09978274

SRNT

Printed 11/17/2004

PA (MINU) UNIV MINNESOTA & RUTGERS.
XX (UYNE-) UNIV STATE NEW JERSEY.
PI Uckun FM, Tumor NE;
XX WPI: 2001-040422/05.
DR P-PSDB: AAR36500.
XX
XX Immunocytotoxic useful for treating cancer and acquired
PT immunodeficiency syndrome, comprises mutant pokeweed anti-viral protein
PT and a targeting moiety that binds a cell surface receptor .
XX
XX Disclosure: Column 47-50; 32pp: English.
XX The present invention describes a fusion protein or an immunocytotoxic
CC amino acid substitution at residue 75, 97 or 176 of native PAP and a
CC targeting moiety that binds a cell surface receptor. (I) can have
CC cytostatic and anti-HIV activities, and is an inhibitor of cellular
CC RNA or protein synthesis. (I) is useful for treating AIDS and cancers
CC including leukaemia, lymphoma, a brain tumour, neuroblastoma,
CC osteosarcoma, soft tissue sarcoma, breast, prostate, ovarian,
CC testicular, melanoma, lung, or colon cancer. Immunocytotoxic prepared
CC using PAP mutants exhibit an improved therapeutic index over
CC immunocytotoxic containing either wild-type PAP or variant PAP.
CC The present sequence encodes the wild-type PAP, which is given in
CC the exemplification of the present invention.
XX
XX Sequence 1379 BP: 488 A; 234 C; 268 G; 389 T; 0 other;
SQ
Query Match 3.1%; Score 29; DB 22; Length 1379;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 915 TAATCTTGGTGATCTATTGAAGGATCT 943
Db 1136 TAATCTTGGTGATCTATTGAAGGATCT 1164
RESULT 8
AAT99556
JD AAT99556 standard: DNA: 882 BP.
XX
XX AAT99556;
XX
XX 08-JUN-1998 (first entry)
XX
XX Phytolacca insularis antiviral protein gPIR2 gene.
XX
XX Antiviral protein: gPIR2 gene; virucide: transgenic plant;
KW virus resistance; immunocytotoxic; AIDS; cancer; therapy; ss.
XX
XX Phytolacca insularis Nakal.
XX
XX Key Location/Qualifiers
FH CDS 1..882
FT FT
FT FT
FT FT
XX
XX EP808902-A2.
XX
XX 26-NOV-1997.
XX
XX 30-SEP-1996; 96EP-0307159.
XX
XX 22-MAY-1996; 96KK-0017404.
XX
XX (JINR-) JIN RO 13D.
XX
XX Choi J, Choi K, Choi Y, Hong E, Jin J, Kim C;
PI Kim M, Lee J, Lee J, Moon Y, Song S, Yun Y;
XX WPI: 1998-001788/01.
DR

09978274

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTTCAAGGATCT 943
 |||||
 Db 944 TAATCTGGTGATCTATTTCAAGGATCT 972

RESULT 4

AAZ59220
 ID AAZ59220 standard; CDNA; 1379 BP.

XX AC AAZ59220;

XX DT 20-APR-2000 (first entry)

XX DE Pokeweed antiviral protein coding sequence spring leaf form.

XX DE Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
 resistance; potato virus X; potato virus Y; potato leaf roll virus;
 tuber; ss.

XX OS Phytolacca americana.

XX PN US6015940-A.

XX PD 18-JAN-2000.

XX PF 07-APR-1992; 92US-0865169.

XX PR 07-APR-1992; 92US-0865169.

XX PA (MONS) MONSANTO CO.

XX PI Kaniewski WK, Turner NE, Lodge JK;

XX DR WPI: 2000-126326/11.

XX PT Production of transgenic potato plants or tubers expressing pokeweed
 antiviral protein which are resistant to potato virus X or Y.

XX PS Claim 6; Fig 4; 30pp; English.

XX CC This is the coding sequence for the spring leaf form of the pokeweed
 antiviral protein (PAP) which is used to generate transgenic potato
 plants. PAP is able to confer resistance to infection by potato virus
 X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
 the potato plant or tuber expressing PAP.

XX SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 other;

Query Match 3.1%; Score 29; DB 21; Length 1379;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTTCAAGGATCT 943
 |||||
 Db 1136 TAATCTGGTGATCTATTTCAAGGATCT 1164

RESULT 5

AAZ59221
 ID AAZ59221 standard; CDNA; 1379 BP.

XX AC AAZ59221;

XX DT 20-APR-2000 (first entry)

XX DE Variant pokeweed antiviral protein spring leaf form coding sequence.

XX DE Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
 resistance; potato virus X; potato virus Y; potato leaf roll virus;
 tuber; ss.

XX

OS Phytolacca americana.

XX PN US6015940-A.

XX PD 18-JAN-2000.

XX PF 07-APR-1992; 92US-0865169.

XX PR 07-APR-1992; 92US-0865169.

XX PA (MONS) MONSANTO CO.

XX PI Kaniewski WK, Turner NE, Lodge JK;

XX DR WPI: 2000-126326/11.

XX PT Production of transgenic potato plants or tubers expressing pokeweed
 antiviral protein which are resistant to potato virus X or Y.

XX PS Claim 7; Fig 5; 30pp; English.

XX CC This is the coding sequence for a variant spring leaf form of the
 pokeweed antiviral protein (PAP) which is used to generate transgenic
 potato plants. PAP is able to confer resistance to infection by potato
 virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV)
 in the potato plant or tuber expressing PAP. PAP varies from PAP
 (AAZ59220) by mutations L20R and Y49H.

XX SO Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 other;

Query Match 3.1%; Score 29; DB 21; Length 1379;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTGGTGATCTATTTCAAGGATCT 943

|||||

Db 1136 TAATCTGGTGATCTATTTCAAGGATCT 1164

RESULT 6

AAZ45197

ID AAZ45197 standard; DNA; 1379 BP.

XX AC AAZ45197;

XX DT 29-FEB-2000 (first entry)

XX DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.

XX DE Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
 ribosome inhibiting protein; RIB; cereal crop; viral resistance; PVX;
 potato virus X; cucumber mosaic virus; CMV; ss;
 tomato yellow leaf curl virus.

XX OS Phytolacca americana.

XX FH Key Location/Qualifiers

XX CDS 225..1166

XX FT /*tag=

XX FT /product= PAP

XX FT /note= "Pokeweed antiviral protein"

XX PN WO9960843-A1.

XX PD 02-DEC-1999.

XX PF 21-MAY-1999; 99WO-US11301.

XX PR 22-MAY-1998; 98US-0086374.

XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX PI Turner NE, Wang P;

SRNT

Printed 11/17/2004

01-JUN-1993.
XX
XX
PF 20-NOV-1991: 91JP-0329672.
XX
PR 20-NOV-1991: 91JP-0329672.
XX
XX (NISB) JAPAN TOBACCO INC.
XX
XX WPI: 1993-211306/26.
DR P-PSDB: AAR37345.
XX
XX New pokeweed antiviral protein (PAP) with similar activity to
PT ricin - used to treat cancer and as an agricultural chemical
XX
XX Claim 2: Page 11-13: 14pp: Japanese.
XX
XX PAP has a similar activity to ricin, i.e. inhibits protein synthesis.
CC The protein may be obtained all year round by recombinant DNA
CC techniques. PAP can be used partic. against cancer and as an
CC agricultural chemical.
CC Total mRNA, is extracted from the seeds, leaves and roots of
CC pokeweed and used to prepare cDNA using PCR. The resultant cDNA is
CC used to prepare two DNA fractions, which are introduced into a
CC cloning vector EMBL3 and then into host E.coli PLK-17 (P2) to
CC produce PAP.
XX
XX Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 other:

Query Match 3.4%; Score 32; DB 14; Length 2472;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 577 GTAGCCATCCAAATGGTTTCAGAGCGCG 608
Db 1587 GTAGCCATCCAAATGGTTTCAGAGCGCG 1618

RESULT 2
AAQ56672
ID AAQ56672 standard; cDNA; 1195 BP.
XX
AC AAQ56672:
XX
XX 04-SEP-1994 (first entry)
XX
XX Sequence of Phytolacca antiviral protein (PAP) cDNA.
DE
XX Antiviral protein: PAP; virus-resistance; transgenic plant: ss.

Phytolacca americana L.
XX
XX Key Location/Qualifiers
FT CDS 33..974
FT /*tag- a
XX
XX EP585554-A.
PN
XX
XX 09-MAR-1994.
PD
XX
XX 30-JUN-1993: 93EP-0110445.
PF
XX 16-AUG-1992: 92KR-0014895.
PR
XX (JINR-) JIN RO LTD.
PA (SHIN-) SHINRO KK.
XX
XX Choi K, Jeong H, Jeong H, Kim M, Lee K, Moon Y;
PI Na B;
XX
XX WPI: 1994-076002/10.
DR P-PSDB: AAR48548.
XX
XX Expression vector for phytolacca antiviral protein - used for

PT producing transgenic virus-resistant plants and for producing the
PT antiviral agent
XX
XX Disclosure: Fig 1: 15pp: English.
XX
XX To isolate PAP gene, total cellular mRNA was purified from leaves of
CC Phytolacca americana L. Obtd. in Korea. A cDNA library was
CC constructed. The PAP gene was selected by immunoscreening employing
CC anti-PAP antibody. A deletion mutant was prepd. from the isolated
CC PAP gene, and the DNA sequence of the PAP genome was determined.
XX
XX Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 other:

Query Match 3.1%; Score 29; DB 15; Length 1195;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 915 TAATCTTGGTGCATCTATTTCAGAGTACT 943
Db 944 TAATCTTGGTGCATCTATTTCAGAGTACT 972

RESULT 3
AAQ81457
ID AAQ81457 standard; cDNA; 1195 BP.
XX
AC AAQ81457:
XX
XX 25-AUG-1995 (first entry)
XX
XX Phytolacca antiviral protein (PAP) cDNA.
DE
XX Antiviral protein: vector pMJ12; KCCM 10037; PAP; ss.

Phytolacca americana L.
XX
PN A09350642-A.
XX
XX 19-JAN-1995.
XX
XX 11-NOV-1993: 93AU-0050642.
XX
XX 02-JUL-1993: 93KR-0012360.
PR
XX (JINR-) JIN RO LTD.
XX
XX Hong-seob J, Kwan-ho L, Kyu-whan C, Man-keun K;
PI Young-ho M, Choi K, Jeon H, Kim M, Lee K, Moon Y;
XX
XX WPI: 1995-067518/10.
DR
XX Recombinant vector for producing Phytolacca anti-viral protein
PT and transformed E. coli useful for making immunconjugates for
PT treatment of AIDS
XX
XX Claim 1: Fig 1: 27pp: English.

Total cellular mRNA from leaves of P. americana was used to produce
a cDNA library and this screened with anti-PAP antibody raised in
rabbits against purified PAP. Inserts were isolated from 2 clones
and sequenced to identify a 1195 ORF (AAQ81457) that encodes a 313 AA
PAP including a 22 AA signal peptide. The mature PAP gene was
subjected to PCR amplification using primers AAO81458 and AAO81459. The
amplification product was cut with Hind III and inserted into the
commercial FLAG (Rm) vector cut with the same enzyme to form pMJ12.
pMJ12 is deposited with the Korean Collection of Culture and
Microorganism (KCCM), an International Depository Authority, on
June 30 1993, ad deposition No. KCCM 10037, and claimed.

Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 other:
Query Match 3.1%; Score 29; DB 16; Length 1195;
Best Local Similarity 100.0%; Pred. No. 0.00022;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2003, 01:16:18 : Search time 292 seconds
(without alignments)
7288.145 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

Sequence: 1 atgaaggtgatgtttagt.....atctatttgaaggatcttaa 945

Scoring table: OLIGO-NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	3.4	2472	14 AAQ43967	Pokeweed antiviral
2	29	3.1	1195	15 AAQ56672	Sequence of Phytol
3	29	3.1	1195	16 AAQ81457	Phytolacca antiviral
4	29	3.1	1379	21 AA259220	Pokeweed antiviral
5	29	3.1	1379	21 AA259221	Variant pokeweed a
6	29	3.1	1379	21 AA245197	Wild-type pokeweed
7	29	3.1	1379	22 AAC87929	P. americana pokew
8	23	2.4	882	19 AAT99556	Phytolacca insular
9	22	2.3	918	15 AAQ64893	Antiviral protein

10	22	2.3	918	16 AAT04782	DNA pJM201 fragme
11	22	2.3	2369	19 AAT99557	Phytolacca insular
12	22	2.3	2369	20 ABA96543	Phytolacca insular
13	22	2.1	1956	20 AAX81493	DNA sequence of cr
14	20	2.1	1956	20 AAX81495	DNA sequence of cr
15	20	2.1	1956	20 AAX81496	DNA sequence of cr
16	20	2.1	1959	20 AAX81532	DNA sequence of cr
17	20	2.1	1959	20 AAX81528	DNA sequence of cr
18	20	2.1	1959	20 AAX81527	DNA sequence of cr
19	20	2.1	1959	20 AAX81498	DNA sequence of cr
20	20	2.1	1959	20 AAX81499	DNA sequence of cr
21	20	2.1	1959	20 AAX81500	DNA sequence of cr
22	20	2.1	1959	20 AAX81501	DNA sequence of cr
23	20	2.1	1959	20 AAX81481	DNA sequence of cr
24	20	2.1	1959	20 AAX81482	DNA sequence of cr
25	20	2.1	1959	20 AAX81483	DNA sequence of cr
26	20	2.1	1959	20 AAX81484	DNA sequence of cr
27	20	2.1	1959	20 AAX81485	DNA sequence of cr
28	20	2.1	1959	20 AAX81486	DNA sequence of cr
29	20	2.1	1959	20 AAX81487	DNA sequence of cr
30	20	2.1	1959	20 AAX81488	DNA sequence of cr
31	20	2.1	1959	20 AAX81489	DNA sequence of cr
32	20	2.1	1959	20 AAX81490	DNA sequence of cr
33	20	2.1	1959	20 AAX81491	DNA sequence of cr
34	20	2.1	1959	20 AAX81492	DNA sequence of cr
35	20	2.1	1959	20 AAX81494	DNA sequence of cr
36	20	2.1	1959	20 AAX81470	DNA sequence of cr
37	20	2.1	1959	20 AAX81471	DNA sequence of cr
38	20	2.1	1959	20 AAX81472	DNA sequence of cr
39	20	2.1	1959	20 AAX81473	DNA sequence of cr
40	20	2.1	1959	20 AAX81474	DNA sequence of cr
41	20	2.1	1959	20 AAX81475	DNA sequence of cr
42	20	2.1	1959	20 AAX81476	DNA sequence of cr
43	20	2.1	1959	20 AAX81477	DNA sequence of cr
44	20	2.1	1959	20 AAX81478	DNA sequence of cr
45	20	2.1	1959	20 AAX81479	DNA sequence of cr

ALIGNMENTS

RESULT 1
AAQ43967
JD AAQ43967 standard; DNA: 2472 BP.
XX
AC AAQ43967;
XX
DT 09-NOV-1993 (first entry)
XX
DE Pokeweed antiviral protein.
XX
KW POKEROOT; ricin; protein synthesis inhibitor; cancer;
XX polymerase chain reaction; PCR; NS.
OS Phytolacca americana.
XX
FH Key
FT CAAT_signal Location/Qualifiers
FT 549...552
FT CAAT_signal /tag= a
FT 627...630 /tag= b
FT TATA_signal 845...850 /tag= c
FT sig_peptide 1014...1085 /tag= d
FT mat_peptide 1086...1868 /tag= e
FT polyA_signal /label= PAP
FT 2130...2135 /tag= f
XX JP05137580-A.
XX

GenCore version 5.1.6
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Gen nucleic - nucleic search, using sw model

Run on: June 2, 2003, 01:15:17 ; Search time 62 Seconds
(without alignments)
4674.347 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

Sequence: 1 atgaaggtagctgtgtagt.....atctatttgaaggattctaa 945

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	634	67.1	1195	1	US-08-373-858-1		Sequence 1, Appli
2	634	67.1	1195	1	US-08-342-786B-1		Sequence 1, Appli
3	632.4	66.9	1379	1	US-08-500-611-1		Sequence 1, Appli
4	632.4	66.9	1379	2	US-08-500-694-1		Sequence 1, Appli
5	632.4	66.9	1379	3	US-07-865-169-1		Sequence 1, Appli
6	632.4	66.9	1379	3	US-09-005-273-1		Sequence 1, Appli
7	632.4	66.9	1379	5	PCT-US96-11546-1		Sequence 1, Appli
8	630.8	66.8	1379	3	US-08-501-253A-1		Sequence 1, Appli
9	629.2	66.6	1379	3	US-07-865-169-2		Sequence 2, Appli
10	629.2	66.6	1379	3	US-09-005-273-3		Sequence 3, Appli
11	543.8	57.5	918	1	US-08-138-636-1		Sequence 1, Appli
12	543.8	57.5	918	1	US-08-319-622A-1		Sequence 1, Appli
13	543.8	57.5	918	1	US-08-471-564-1		Sequence 1, Appli
14	88.4	9.4	804	2	US-08-356-161-6		Sequence 6, Appli
15	88.4	9.4	804	2	US-08-356-161-7		Sequence 7, Appli
16	88.4	9.4	804	3	US-08-718-904-22		Sequence 22, Appli
17	88.4	9.4	804	3	US-08-718-904-23		Sequence 23, Appli
18	88.4	9.4	804	5	PCT-US93-05702-6		Sequence 6, Appli
19	88.4	9.4	804	5	PCT-US93-05702-7		Sequence 7, Appli
20	88.4	9.4	804	5	PCT-US95-10973A-6		Sequence 6, Appli
21	88.4	9.4	804	5	PCT-US95-10973A-7		Sequence 7, Appli
22	88.2	9.3	774	5	PCT-US91-05766-1		Sequence 1, Appli
23	82	8.7	804	2	US-08-356-161-4		Sequence 4, Appli
24	82	8.7	804	3	US-08-718-904-20		Sequence 20, Appli
25	82	8.7	804	5	PCT-US93-05702-4		Sequence 4, Appli
26	82	8.7	804	5	PCT-US95-10973A-4		Sequence 4, Appli
27	80.4	8.5	804	2	US-08-356-161-3		Sequence 3, Appli

Sequence 5, Appli
Sequence 14, Appli
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Sequence 11, Appli
Sequence 246, App

ALIGNMENTS

RESULT 1
US-08-373-858-1
Sequence 1, Application US/08373858
Patent No. 5633155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwun-Ho
APPLICANT: Na, Byong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytolacca
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
TITLE OF INVENTION: Plant Transformed Thereof.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSED: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373.858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELEPHONE: 212-527-7770
TELEFAX: 212-527-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

209 ACCAATGCTGCCCAATACAAATACAAATCCAAAGTAGCTGTGGTTGAGCTCCAAAGTTTC 268
243 AACCTAAAACACATACACTAATGCTGAGAGAAATAACTTATACCTGATGGCTATTTC 302
269 AATATAAAACACATACACTAATGCTGAGAGAAACAAATTTGATGCTGATGGTTATTTC 328
303 TGATCCCTTCAATGGCAATAGTGTGCTTACCATAATATTTAATGATATTTACAAGCAGCGA 362
329 TGATCCCTTTCAAAACCAATAAATGCTGTTACCATATCTTTAATGATATCTCAGGTACTGA 388
363 AGGCATGATGTCGAGATACTCTTCTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 422
389 AGGCAAGATGATAGAGACTACTCTTTGGCCAAATGCCCAATTTCTGCTGCTGCTGCTGCTGCT 448
423 TAACATAACATACCTTATATCCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 482
449 AACTTTGATAGTGCATATCAACATTTGGAATCAAAAGCGGAGTAAATCAAGAAGTCA 508
483 AGTCCAAATGGGAATTCNAATACATCAGAGTGCATTTGGAAAAATCTCTGAGTTGATTC 542
509 AGTCCAACTGGCAATTCNAATACATCAGAGTGCATTTGGAAAAATTTCTGAGTGCATTC 568
543 ATTCCTCTAAACATGAGGCTTTTCTTACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 602
569 ATTCCTAGAGAAACCGAGCGGAAATTCCTATTGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 628
603 AGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGAGCATTCATACC 662
629 AGCAAGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGAGCATTCATACC 688
663 TGATCCCAAGTAAATTTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722
689 TAATCCCAAGTAAATTTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 748
723 TGCCAAAGATGGGCTTTACCCAAACCACTTACAGTGTGAGTGCAGAGTGCAGAGTGCAGAGT 782
749 TGCCAAAGATGGGCTTTACCCAAACCACTTACAGTGTGAGTGCAGAGTGCAGAGTGCAGAGT 808
783 GATAGTCTTGAAGTGGATGAATCAATCAATGATGCTAGTGCAGTGCAGTGCAGTGCAGTGCAG 842
809 GATAGTGTGAGTGGATGAATCAATCAATGATGCTAGTGCAGTGCAGTGCAGTGCAGTGCAGT 868
843 AACCTGTGAGCAACTT---ACCAAAATGCCATGCTCTCAAGTATATTAATTTCTACTTA 899
869 GAGCTGTGAGCAACTTATAACCAAAATGCCATGTTTCTCAACTTATTAATGCTACTTA 928
900 TTATAATATATGCTAATCTTGGTGATCTATTGGAAGGATTTAA 945
929 TTATAATATGCTAATCTTGGTGATCTATTGGAAGGATTTAA 974

RESULT 3
US-08-500-611-1
Sequence 1, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: Poxweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500.611

FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIMS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Query Match 66.9% Score 632.4 DB 1 Length 1379
Best Local Similarity 80.0% Pred. No. 5.8e-169
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1
QY 3 GAAGTGTGCTGCTTGTAGTTGCTGACCTTAATAGCTGGCTCATTCGTGACCAAGTTTC 52
DB 221 GAAGTGAAGTCGATGCTTGTGTCACAAATCAATATGGCTCATTCGTGACCAAGTTTC 280
QY 63 AACTGTGCTCAATAATAGTACCTTTGATGCTGGAAATGCCACCATTAATAANTGCT 122
DB 201 AACTGTGCTGATACAAATCAATCAATGCTGAAAGTACCACCATTAACCAATACGC 340
QY 123 CACTTTTATGGAATCTTTGATATCAAGGAGAGATCCAAATCAATGCTATGCTAT 182
DB 341 CACTTTTATGGAATCTTTGATATCAAGGAGAGATCCAAATCAATGCTATGCTAT 400
QY 183 ACCAATGCTGCTGATGATCAATTCGACCGCTAAGTACTTATTGGTTAAGTTCGAAGTTC 242
DB 401 ACCAATGCTGCTGATGATCAATTCGACCGCTAAGTACTTATTGGTTAAGTTCGAAGTTC 460
QY 243 AAACCTAAACACCATTAACCTAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302
DB 461 AAATAAAACACCATCAACATTAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 520
QY 303 TGATGCTTCAATGCTGATTAAGTGTGCTTACCATATATTTAATGATATTTACCAATGCTA 362
DB 521 TGATGCTTCAATGCTGATTAAGTGTGCTTACCATATATTTAATGATATTTACCAATGCTA 580
QY 363 AGGCATGATGCTGAGATACTCTTCTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 422
DB 581 AGGCATGATGCTGAGATACTCTTCTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 640
QY 423 TAACATAACATACCTTATATCCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 482
DB 641 AACTTTGATAGTGCATATCAACATTTGGAATCAAAAGCGGAGTAAATCAAGAAGTCA 700
QY 483 AGTCCAAATGGGAATTCNAATACATCAGAGTGCATTTGGAAAAATCTCTGAGTTGATTC 542
DB 701 GGTCCAAATGGGAATTCNAATACATCAGAGTGCATTTGGAAAAATCTCTGAGTTGATTC 760
QY 543 ATTCCTCTAAACATGAGGCTTTTCTTACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 602
DB 761 ATTCCTCTAGAGAAACCGAGCGGAAATTCCTATTGCTAGCTAGCTAGCTAGCTAGCTAGCT 820

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

NAME/KEY: CDS

LOCATION: 225..1163

NAME/KEY: sig_peptide

LOCATION: 225..290

Query Match

Best Local Similarity 80.0% Pred. No. 5.8e-169

Mismatches 757; Conservative 0; Matches 186; Indels 3; Gaps 1;

QY	3	GAAGTGATGCTTGTGTGCTGACGTTAATAGGCTGCTCATTCGCTGCACCAACTTC	62
DB	221	GAAGATGAAGTCGATGCTTGTGTGACATATCAATATGCTCATTCCTCCACCACTTC	280
QY	63	AACTTGCGCATTAATACGATCACTTTGATGCTGGAATGCGACCAATTAACAATATGC	122
DB	281	AACTTGCGCATTAATACGATCACTTTGATGCTGGAATGCGACCAATTAACAATATGC	340
QY	123	CACCTTTATGGAATCTCTTCGTAATCAACGGAAGATCCAAACTAAATGCTATGGCAT	182
DB	341	CACCTTTATGGAATCTCTTCGTAATCAACGGAAGATCCAAACTAAATGCTATGGCAT	400
QY	183	ACCAATGCTACCTGATACCTTTATTCGACCCCTAAGTACTTATTGGTTAAGCTCAAGGTCC	242
DB	401	ACCAATGCTACCTGATACCTTTATTCGACCCCTAAGTACTTATTGGTTAAGCTCAAGGTCC	460
QY	243	AAACCTAAACCACTTACACTATCTGCTGAGAGAAATCACTTATACGCTATGGGTATTC	302
DB	461	AAACCTAAACCACTTACACTATCTGCTGAGAGAAATCACTTATACGCTATGGGTATTC	520
QY	303	TGATCCCTTCAATGGCAATAGTCTGTTTACCATATATTAATGATATTACAGCACCA	362
DB	521	TGATCCCTTCAATGGCAATAGTCTGTTTACCATATATTAATGATATTACAGCACCA	580
QY	363	ACGCACTGATGAGAGATACCTTTTGTCTCAAGTCTTCTGCTGTTGCAATGTCCAT	422
DB	581	ACGCACTGATGAGAGATACCTTTTGTCTCAAGTCTTCTGCTGTTGCAATGTCCAT	640
QY	423	TAACTACATACCTTATATCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	482
DB	641	TAACTACATACCTTATATCCCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	700
QY	483	AGTCAATTTGGGAATCAAAATCTCAGGAGTACATTTGGAAGAGAGAGAGAGAGAG	542
DB	701	AGTCAATTTGGGAATCAAAATCTCAGGAGTACATTTGGAAGAGAGAGAGAGAGAG	760
QY	543	ATTCCCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	602
DB	761	ATTCCCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	820
QY	603	AGCGGCTTCAAGTACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	662
DB	821	AGCGGCTTCAAGTACATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	880
QY	663	TGATCCCAAGTAAATTAATTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	722
DB	881	TGATCCCAAGTAAATTAATTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	940

QY	723	TGCCAAGAATGGGCTTTTACCCAAACCACTTTGAGCTAGTGATGCCAAAGGATCCAAAGTG	782
DB	941	TGCCAAGAATGGGCTTTTACCCAAACCACTTTGAGCTAGTGATGCCAAAGGATCCAAAGTG	1000
QY	783	GATAGTCTTTCAGAGTGGATGAAATCAATCGTATGTCGACCTCCCTTAAGTACTTAAATG	842
DB	1001	GATAGTCTTTCAGAGTGGATGAAATCAATCGTATGTCGACCTCCCTTAAGTACTTAAATG	1060
QY	843	AACTCTCAGACCAACTT---ACCAAAATGCCATGTTCTCTCAAGTTATATTTTAACTTA	899
DB	1061	AACTCTCAGACCAACTT---ACCAAAATGCCATGTTCTCTCAAGTTATATTTTAACTTA	1120
QY	900	TTATAATTATATCTCTAAATCTTGGTATCTATTTGAAGGATTCCTAA	945
DB	1121	TTATAATTATATCTCTAAATCTTGGTATCTATTTGAAGGATTCCTAA	1166

RESULT 7

PCT-US96-11546-1

Sequence 1: Application PC/TUS9611546

GENERAL INFORMATION:

APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik

STREET: 600 South Avenue West

CITY: Westfield

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/11546

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/500,694

FILING DATE: 11-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REFERENCE/DOCKET NUMBER: OCIRS 3.0-039

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000

TELEFAX: 908-654-7866

TELEX: 139-125

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 225..1163

FEATURE:

NAME/KEY: mutation

LOCATION: replace(233, "a")

FEATURE:

NAME/KEY: mutation

LOCATION: replace(349, "g")

FEATURE:

NAME/KEY: mutation

LOCATION: replace(435, "c")

PCT-US96-11546-1

Query Match

66.9% Score 632.4; DB 5; Length 1379;

62 GGGCGGTGAATACCATCATCTACCATGTTGGAAAGTACCAACATTAGAAACATATCAACTT 121
128 TTATGGAATCTTTCGTAATCAAGCAAGATCCAAACAACTAAATGCTATGGCATACCAA 187
122 TTGGATA-----CTTCGTACTCAAGCGCAAGATCC--AAGTTATGCTATGGATACCAA 175
188 TGCTACCTGATACATAATTCGACCCCTAAGTACTATTATGGTTAGCTCCAAAGGTCAACG 247
176 TGCTGCCCAATATTGGGATCAATCCAAATACATATTGGTTGAGCTCCAAAGGTTCAATG 235
248 TAAAGACATTACACTAATCTCGAGAGCAATACCTATACGTGATGGGCTATCTGATC 307
236 AAGAGGCATCACACTANTGCTAGAGCAACAATTTATATGATGGGCTATCTGATC 295
308 CTTCAATGGCAATAAGTGTGTTACCATATTTAATGATATATCAAGCACCGAAGCGCA 367
296 CTTACAA--CAATAGTGTGTTTCCATCTCTTAAAGGCTATCTCAGGTACTGACGGC 352
368 CTGATCTGGAGATACCTTTGCTCAAGTCTAGTTCCTGCTGTTGCAATGCTCATTAACT 427
353 AGATGTAGAGACTACTCTTTGCCCCAAATGCCATTCCTGTTGGTAAACATAAACT 412
428 ACAATAGCTTATATCCGACCATCGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCC 487
413 ATGATAGTGCATATCCAACTTGGATCAAGATCAAGAGGATTAATCAAGAAAGTCAAGTCC 472
488 AATTGGGAATCAAACTACTCAGCAGTGACATTTGGAATAATCTCTGGAGTGTGATTCTCC 547
473 AACTGGGAATTCGAATACTCAGCAGTGGAATGGGAAGGATTTCTGGAGTCACTTCA 532
548 CTGTAATAAACTGAGGCTTTTCTTACTGTAGTCCATCCAAATGGTTTCAGAGGCGCGC 607
533 CTGAGAGACCGAAGCTGAATTCCTACTGTAGCCATCAAAATGGTATCAGAGGCGCA 592
608 GATTCAGTACATAGAGAACCAAGTCAAGCACTAATTTAATGAGCATTTCTACCTGATC 667
593 GATTCAGTACATAGAGTCAAGTCAAACTAATTTTACAGACCTTCAACCCCTAATC 652
668 CCAAGTAAATTAATTGGAGGAGAGTGGGGCAAAATCTCTGAGGCAATTCACAATGCCA 727
653 CCAAGTAAATTAATTGGAGGAGAGTGGGGCAAAATCTCTGAGGCAATTCAGTGGTCCA 712
728 AGAATGGGCTTTACCCCAACACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 787
713 GGAATGGAGTTTACCCCAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 772
788 TTCCTAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 847
773 TCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 832
848 GTCAGACAACTT--ACCAAAATGCAATGCTCTCTCAAGTGTATATTTCTACTTATTATA 904
833 GCCAGAGAACTTAAACCAAAATGCAATGCTCTCTCAAGTGTATATTTCTACTTATTATA 892
905 ATTATATGCTAATCTTGGTGTAT 927
893 ATTATATGCTAATCTTGGTGTAT 915

Sequence 6, Application US/08356161
Sequence No. 5916772

GENERAL INFORMATION:

APPLICANT: Leppl, Douglas A.
APPLICANT: Barthelmy, Isabel
APPLICANT: Baird, J. Andrew
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
NUMBER OF INVENTION: SAPORIN-CONTAINING PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP

STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,161
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,161
FILING DATE: 13-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5916772tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.40405
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: mIsC_feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
corresponding to the clone M13 mp18-G7 in Example 1.B.2."
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-356-161-6

Query Match 9.4% Score 88.4; DB 2: Length 804;
Best Local Similarity 49.3%; Pred. No. 1.1e-15;
Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

QY 47 TTGCTGCAACCACTTCAACTGTGTCATATATACATCACCTTTTGTATGCTGCAATGCA 106
DB 20 TTTCAGCTTGGACACAACTGATCGGTGCATCAATCACATTAGATCTGTAATACCA 79
QY 107 CCATTACAAATATGCCACCTTTTATGGAATCTCTTGTAAATCAAGCAAGATCCAAAC 166
DB 80 CCGCGGTCAATCACTCATCTTTTGGATAAATCCGAACACGTAAGGATCAACAC 139
QY 167 TAAATGCTATGGCATACCAATGC---TACCTGATCAATATTCGACCCCTAAGTACTTAT 223
DB 140 TCAATACGGTGTGATACCGCATAGCCGTCATAGCCACCTTCTAAGAAATATCTTA 199
QY 224 TGGTTAAGCTCCAGGTGCAACCTTAAACGATTAATGATGATGATGATGATGATGAT 283
DB 200 GAAITAAITTCGCAAGTTC---CCGAGCAAGCTTCTACTTGGCTTAAACGCAATAC 256
QY 284 TATAGTGTGATGCTTCTGATCCCTTCAATGCAATAGTGTGATGATGATGATGATGAT 343
DB 257 TGTATGCTGCTGCTGATCTTTCGAATGATGATGATGATGATGATGATGATGATGAT 316
QY 344 ATGATATTAACAGCAACGACCACTGATGATGATGATGATGATGATGATGATGATGAT 404
DB 317 GATCAGAAATTAATCTTCCGCGGAGTTAAACCGCTTTTCCGAGAGGCGCACACTG 376

us-09-978-274a-1.rni

Jun 2 10:54:58 2003

404 CTCGTGTTGCAATGTCATTAACATAAGTATATATCCGACCAATGCAAGAAAGACG 463

377 AGAAAGCTTTAGATACACAGAGATTATACAGTCGATCGAAAGAAATGCCCAATACAC 436

454 AAGTA---AATCAAGAAATCAAGTCCAAATTTGGGAATTCAAATACATCACCAGTGACATTG 520

437 ACGGAGATAAATCAAGAAAGAACTCGGTTGGGATCGACTTACTTTTGGAGTCCATCG 496

521 GAAATCTCTGGAGTTGATTCATTCCTCTGTAATAAAGTCAAGGCTTTTCTTACTGCTAG 580

497 AAGCACTGCAACAAGA---AGGCACTGTGGTTTAAAGCAAGCTAGATCTCTTATCG 553

581 CCATCCAAATGGTTTCAGAGGAGCGGATTCAGATACATAGAGAACCAAGTCAAGACTA 640

554 CTATTCAGATGACGCTGAGGACGACGATTAGGTATACATACAAAAGTGGTAATCAAGA 613

641 ATTTTAAATAGACATCTTACCCTGATCCCAAGTAATTAATTTGGAGGAGAACTGGGCA 700

614 ACTTTCCCAACAAGTTCAACTCGGAAACAAAGTATTCAGTTTGAGGTTTAACCTGGAAA 673

701 AATCTCTGAGCAATTCAC---AATGCCAAGAAATGGGCTTTTACCCAAACCACTTGAGC 757

674 AATTTCTACGCAATATACGCGGATGCGCAAAACGCGGTGTTTAAAGATATGATT 733

758 TACTGATGCAAGAGTACCAAGTGGATGATCTTCTAGAGTGG 799

734 TCGGTTTGGAAAGTCAGCGAGTGAAGGACTTGCAATGG 775

us-08-356-161-7

Query Match 9.4% Score 88.4 DB 2: Length 804

Best Local Similarity 49.3% Pied. No. 1.1e-15

Mismatches 376; Conservative 0; Indels 15; Gaps 5

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..804

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..804

OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G9 in Example 1.B.2."

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 46..804

OTHER INFORMATION: /product= "Saporin"

US-08-356-161-7

47 TTGCTGCACCAACTTCAACTTGTGCTCAATAAATACGATCACCTTTGATGCTGCAAAATGCA 106

20 TTTCAGCTTGGCAACAACATGATGCGGTCAATCAATCAATCAATCAATCAATCAATCAAT 79

107 CCATTAACAATAATGCGACCTTTTATGTAATCTCTTCGTAAATCAAGCGAAGATGCAAAAC 166

80 CCGCGGTCAATATCTCATCTTTTGTGATATAAATCCGAAACAAAGTAAAGATGCAAAAC 139

167 TAAATGCTATGCTACCAATGCG---TACCTGATACATTAATTCGACCCCTAAATGATTTAT 223

140 TGAATACGGTGTGATGACATAGCGCTGTAAGGCTCACCTTCTTAAGAAATAATTTCTTA 159

224 TGGTTAAGTCCCAAGGTGAAAGCTTAAAGACATTAACATACTTCTGAGCAAGAAATAACT 283

200 GAATTAATTTCCAAAGTTC---CGGAGCAAGCTGCTCACCTTGGCTTAAAGAGTCAAT 256

284 TATAGCTGATGGGTATTCTGATGCTCTTAAATGCAATAGTGTCTGCTTACCATATATTA 343

257 TGTATCTGCTGGGTATCTTGCATGATGATACAGAAATGTTAATCGGCGCTTATCTTCA 316

344 ATGATATACAGCAAGCAAGCGCACTGATGCGGAGATACCTTTTGTCTCAAGTCTTACT 403

317 GATCAGAAATTAATCTCCGCGGAGTTAGCGCGCTTTTCCAGAGGCGCAATTTCAATC 376

404 CTCGTGTTGCAATGTCATTAACATAAGTATATATCCGACCAATGCAAGAAAGACG 463

377 AGAAAGCTTTAGATACACAGAGATTATACAGTCGATCGAAAGAAATGCCCAATACAC 436

464 AAGTAAGTCA---AGAAATCAAGTCCCAATTTGGGAATTCAAATACATCACCAGTGACATTG 520

437 AAGGATATCAAGTAAAGAAAGTTCGCGTTGGGATTCAGTTCTTCAAGTCTGATG 496

521 GAAATCTCTGGAGTTGATTCATTCCTCTGTAATAAAGTCAAGGCTTTTCTTACTGCTAG 580

497 AAGCACTGCAACAAGA---AGGCACTGTGGTTTAAAGCAAGCTAGATCTCTTATCG 553

581 CCATCCAAATGGTTTCAGAGGAGCGGATTCAGATACATAGAGAACCAAGTCAAGACTA 640

554 CTATTCAGATGACGCTGAGGACGACGATTAGGTATACATACAAAAGTGGTAATCAAGA 613

641 ATTTTAAATAGACATCTTACCCTGATCCCAAGTAATTAATTTGGAGGAGAACTGGGCA 700

614 ACTTTCCCAACAAGTTCAACTCGGAAACAAAGTATTCAGTTTGAGGTTTAACCTGGAAA 673

701 AATCTCTGAGCAATTCAC---AATGCCAAGAAATGGGCTTTTACCCAAACCACTTGAGC 757

674 AATTTCTACGCAATATACGCGGATGCGCAAAACGCGGTGTTTAAAGATATGATT 733

758 TACTGATGCAAGAGTACCAAGTGGATGATCTTCTAGAGTGG 799

734 TCGGTTTGGAAAGTCAGCGAGTGAAGGACTTGCAATGG 775

Mon Jun 2 10:54:58 2003

time : 65 secs

us-09-978-274a-1.rni

Page 14

06/02/2003

137

SRNT

Printed 11/17/2004

09978274

GenCore version 5.1.4_p5-4578
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protein - protein search, using sw model

Run on: May 28, 2003, 09:59:45 ; Search time 25 Seconds
(without alignments)
520.943 Million cell updates/sec

Title: US-09-978-274A-2

Perfect score: 314

Sequence: 1 MKVNLVVVTLIAWLAAPT.....VLIISTYNNMNLGDLPEGF 314

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	10.2	294	1	RIPA-PHYAM
2	30	9.6	313	1	RIP1-PHYAM
3	28	8.9	261	1	RIPS-PHYAM
4	14	4.5	278	1	RIPP-MIRSA
5	11	3.5	282	1	RIP2-BRIDI
6	10	3.2	32	1	RIP2-PHYDI
7	10	3.2	316	1	RIPG-GELMU
8	10	3.2	563	1	RIPG-SAMMI
9	9	2.9	286	1	RIP1-MOMCH
10	9	2.9	286	1	RIP2-MOMBA
11	8	2.5	272	1	FAIL-RHINE
12	7	2.2	130	1	PFDA-THEVO
13	7	2.2	132	1	TVAS3-THOUSE
14	7	2.2	258	1	YURA-MYXXA
15	7	2.2	275	1	FA9-RABIT
16	7	2.2	282	1	FA9-RAT
17	7	2.2	300	1	ARGB-BRUNE
18	7	2.2	310	1	RIP2-PHYAM
19	7	2.2	319	1	SYGA-COXBU
20	7	2.2	321	1	HIQA-ARATH
21	7	2.2	384	1	CGB3-CAEEL
22	7	2.2	422	1	VUS3-YEAST
23	7	2.2	429	1	YNO5-MYCTU
24	7	2.2	452	1	FA9-CANFA
25	7	2.2	459	1	FA9-MOUSE
26	7	2.2	507	1	ATPA-MAIZE
27	7	2.2	569	1	AMP2-LYCES
28	7	2.2	607	1	SYRC-YEAST
29	7	2.2	627	1	HEN1-OPSTA
30	7	2.2	743	1	TEF3-HUMAN
31	7	2.2	893	1	PER-PERAM
32	7	2.2	954	1	FLEY-CAUCR
33	7	2.2	990	1	T3RE-SALTY

34 7 2.2 1128 1 PHVA-ORYSA
35 7 2.2 1522 1 DNA2-YEAST
36 7 2.2 3591 1 PHAB-BORPE
37 7 2.2 3707 1 PGBM-MOUSE
38 6 1.9 19 1 OXLA-OPHUA
39 6 1.9 62 1 CYHL-MAJKA
40 6 1.9 70 1 Y3C4-STWCO
41 6 1.9 73 1 VP04-RPAPS
42 6 1.9 76 1 TXP4-APTSC
43 6 1.9 76 1 TXP6-APTSC
44 6 1.9 78 1 GLPE-HUMAN
45 6 1.9 79 1 CMCL-ETNAC

ALIGNMENTS

RESULT 1

RIPA-PHYAM
ID RIPA-PHYAM STANDARD: PRI: 294 AA.

AC G03464;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein alpha precursor (PAP-alpha) (Ribosome-inactivating protein) (rRNA N-glycosidase) (EC 3.2.2.22).
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Caryophyllaceae; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed, Leaf, and Root;
RX MEDLINE=93099240; PubMed=1281438;
RA Kataoka J., Habuka N., Masuta C., Miyano M., Koizumi A.;
RT "Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein...";
RL Plant Mol. Biol. 20:879-886(1992).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=95010127; PubMed=7925458;
RA Ago H., Kataoka J., Tsuge H., Hahuba N., Inagaki E., Noma M., Miyano M.;
RT "X-ray structure of a pokeweed antiviral protein, coded by a new genomic clone, at 0.23-nm resolution. A model structure provides a suitable electrostatic field for substrate binding.";
RL Eur. J. Biochem. 225:369-374(1994).
CC -!- SYNTHESIS IN VITRO. HAS ALSO BEEN SHOWN TO INHIBIT THE REPLICATION OF MAMMALIAN VIRUSES. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR SUICIDE UPON INVASION BY A VIRUS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.

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EMBL: D10600; BAA01451.1;
PIR: S28421; S28421.
PDB: LAPA; 3I-JAN-94.
InterPro: IPR001574; RIP.
Pfam: PF00161; RIP; 1.
PROSITE: P500275; SHIGA_RICIN; 1.

Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase;

Toxin; Signal; Cell wall; 3D-structure

SIGNAL 1 24

CHAIN 25 285

PROPEP 286 294

ACT_SITE 199 199

DISULFID 58 282

FT DISULFID 108 130

FT STRAND 28 31

FT HELIX 32 34

FT STRAND 37 51

FT STRAND 57 58

FT TURN 59 60

FT STRAND 61 63

FT TURN 67 68

FT STRAND 73 79

FT TURN 81 82

FT STRAND 85 91

FT TURN 92 94

FT STRAND 97 104

FT TURN 105 106

FT STRAND 107 113

FT TURN 114 115

FT HELIX 119 129

FT STRAND 136 138

FT STRAND 141 141

FT HELIX 147 154

FT TURN 155 155

FT HELIX 158 160

FT STRAND 163 163

FT HELIX 165 175

FT TURN 176 177

FT HELIX 183 195

FT TURN 196 197

FT HELIX 198 202

FT TURN 213 215

FT STRAND 218 218

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FT HELIX 265 271

FT STRAND 275 275

SQ SEQUENCE 294 AA: 33069 MW: 72627724FA85596 CRC64;

Query Match 10.2% Score 32; DB 1; Length 294;

Best Local Similarity 100.0%; Pred. No. 28-25;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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190 FLVATOMVSEARFKYIENQVKTNRFP 221

189 FLVATOMVSEARFKYIENQVKTNRFP 220

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189 FLVATOMVSEARFKYIENQVKTNRFP 220

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189 FLVATOMVSEARFKYIENQVKTNRFP 220

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189 FLVATOMVSEARFKYIENQVKTNRFP 220

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189 FLVATOMVSEARFKYIENQVKTNRFP 220

SEQUENCE FROM N.A., AND SEQUENCE OF 23-62.

TISSUE=Leaf;

MEDLINE=92003676; PubMed=1912488;

Lin Q., Chen Z.C., Antoniw J.F., White R.F.;

"Isolation and characterization of a cDNA clone encoding the

anti-viral protein from *Phytolacca americana*.";

Plant Mol. Biol. 17:609-614(1991).

[2]

SEQUENCE OF 23-65.

MEDLINE=89193489; PubMed=2930487;

Barbieri L., Bolognesi A., Centini P., Falasca A.I., Minghetti A.,

Carofano L., Guicciardi A., Lappi D., Miller S.P.;

"Ribosome-inactivating proteins from plant cells in culture.";

Biochem. J. 257:801-807(1989).

[3]

SEQUENCE OF 23-54.

TISSUE=Leaf;

MEDLINE=83290867; PubMed=6885760;

Houston L.L., Ramakrishnan S., Hermodson M.A.;

"Seasonal variations in different forms of pokeweed antiviral protein,

a potent inactivator of ribosomes.";

J. Biol. Chem. 258:9601-9604(1983).

[4]

SEQUENCE OF 23-54.

TISSUE=Leaf;

MEDLINE=85023392; PubMed=6091760;

Bjorn M.J., Larlick J., Platak M., Wilson K.J.;

"Characterization of translational inhibitors from *Phytolacca*

americana: amino-terminal sequence determination and antibody-

inhibitor conjugates.";

Biochim. Biophys. Acta 790:154-163(1984).

[5]

SEQUENCE OF 23-54.

TISSUE=Root;

MEDLINE=91064383; PubMed=2248976;

Bolognesi A., Barbieri L., Abbondanza A., Falasca A.I., Carnicelli D.,

Battelli M.G., Stirpe F.;

"Purification and properties of new ribosome-inactivating proteins

with RNA N-glycosidase activity.";

Biochim. Biophys. Acta 1087:293-302(1990).

[6]

X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

MEDLINE=94016586; PubMed=8411176;

Monzingo A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D.;

"The 2.5 A structure of pokeweed antiviral protein.";

J. Mol. Biol. 233:705-715(1993).

[7]

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-284.

MEDLINE=99421320; PubMed=10493577;

Kurinov I.V., Myers D.E., Irvin J.D., Uckun F.M.;

"X-ray crystallographic analysis of the structural basis for the

interactions of pokeweed antiviral protein with its active site

inhibitor and ribosomal RNA substrate analogs.";

Protein Sci. 8:1765-1772(1999).

CC -!- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN

SYNTHESIS IN VITRO.

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

specific adenosine on the 28S rRNA.

CC -!- TISSUE SPECIFICITY: SPRING LEAVES AND ROOTS.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUBFAMILY.

CC -----

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the European Bioinformatics Institute. There are no restrictions on its

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or send an email to license@isb-sib.ch).

CC -----

DR EMBL: X55383; CAA39054.1;

DR PIR: S02792; S02792.

DR PIR: S13469; S13469.

DR

DR

DR

DR

DR

DR

POB: LPAC: 31-JAN-94.
POB: LPAC: 31-JAN-94.
POB: LOCI: 15-SEP-99.
POB: LOCI: 15-SEP-99.
POB: LOCI: 15-SEP-99.
POB: LOCI: 15-SEP-99.
InterPro: IPR001574; RIP.
Pfam: PFO0161; RIP.
PRINTS: PR00396; SHIGARICIN.
PROSITE: PS00275; SHIGA_RICIN; 1.
Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase.
Toxin: Signal; 3D-structure.
CHAIN 1 22 ANTIVIRAL PROTEIN I.
FT PROPEP 23 285
FT ACT_SITE 286 313
FT ACT_SITE 198 198
FT DISULFID 56 281
FT DISULFID 107 128
FT STRAND 25 29
FT STRAND 35 49
FT STRAND 55 56
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FT STRAND 254 255
FT STRAND 258 263
FT STRAND 264 270
FT STRAND 274 274
SEQUENCE 313 AA: 35219 MW: 2C57B2861EBA57F5 CRC64:

ANTIVIRAL PROTEIN I.

BY SIMILARITY.

DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein S (PAP-S) (Ribosome-inactivating protein) (rRNA
DE N-glycosidase) (EC 3.2.2.22).
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Magnoliophyta: Phytolaccaceae: Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=91242096; PubMed=1368643;
RA Kung S.S., Kimura M., Funatsu G.;
RT "The complete amino acid sequence of antiviral protein from the seeds
RT of pokeweed (Phytolacca americana).";
RL Agric. Biol. Chem. 54:3301-3318(1990).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
CC SYNTHESIS IN VITRO.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
DR PIR: JEO401; JEO401.
DR HSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PFO0161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin.
FT ACT_SITE 175 175 BY SIMILARITY.
FT DISULFID 34 258
FT DISULFID 84 105
SQ SEQUENCE 261 AA: 25200 MW: D88H99962FE8399D CRC64:

Query Match 8.9% Score 28; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. NO. 2.6e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 150 FLVAIQMVSEAAEFKYIENQVKTENR 217
DB 165 FLVAIQMVSEAAEFKYIENQVKTENR 192

RESULT 4

RIPP_MIRJA
ID RIPP_MIRJA STANDARD; PRT: 278 AA.
AC P21326;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein MAP precursor (Ribosome-inactivating protein) (rRNA
DE N-glycosidase) (EC 3.2.2.22).
OS Mirabilis jalapa (Jardén four-o'clock).
OC Eukaryota: Viridiplantae: Streptophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Magnoliophyta: Nyctaginaceae: Mirabilis.
OX NCBI_TaxID=3538;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91217082; PubMed=2022657;
RA Kataoka J., Habuka N., Furuno M., Miyano M., Takenami Y., Koiwai A.;
RT "DNA sequence of Mirabilis antiviral protein (MAP), a ribosome-
RT inactivating protein with an antiviral property, from mirabilis
RT jalapa L. and its expression in Escherichia coli.";
RL J. Biol. Chem. 266:8426-8430(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93107126; PubMed=8451171;
RA Kataoka J., Miyano M., Habuka N., Masura C., Koiwai A.;
RT "A genomic gene for MAP, a ribosome-inactivating protein from
RT Mirabilis jalapa, contains an intron.";
RL Nucleic Acids Res. 21:1035-1035(1993).

Query Match 9.6% Score 30; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. NO. 2.6e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Caps 0;

190 FLVAIQMVSEAAEFKYIENQVKTENRAF 219
188 FLVAIQMVSEAAEFKYIENQVKTENRAF 217

RESULT 3

RIPS_PHYAM
ID RIPS_PHYAM STANDARD; PRT: 261 AA.
AC P23339;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)

[3]
SEQUENCE OF 29-278.
MEDLINE-89214063: Pubmed-2708128;
Habuka N., Murakami Y., Noma M., Kudo T., Horikoshi K.;
"Amino acid sequence of Mirabilis antiviral protein, total synthesis
of its gene and expression in Escherichia coli.";
J. Biol. Chem. 264:6629-6637(1989).
CC -!- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
SYNTHESIS IN VITRO.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: D10227; BAA01079.1; -
CC EMBL: D10369; BAA01425.1; -
CC PIR: A39817; A39817.
CC PIR: S36928; S36928.
CC HSSP: Q03464; IAPA.
CC InterPro: IPR001574; RIP.
CC Pfam: PF00161; RIP. 1.
CC PRINTS: PR00396; SHIGARICIN.
CC PROSITE: PS00275; SHIGA_RICIN; 1.
CC Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 28
FT CHAIN 29 278 ANTIVIRAL PROTEIN MAP.
FT ACT_SITE 196 196 BY SIMILARITY.
FT DISULFID 64 248 POTENTIAL.
FT CONFLICT 35 35 I -> L (IN REF. 1).
FT CONFLICT 58 58 A -> V (IN REF. 1).
FT CONFLICT 180 180 V -> C (IN REF. 1).
FT CONFLICT 218 218 D -> G (IN REF. 1).
FT CONFLICT 278 278 BDB9E08E65D2F92D CRC64;
SQ SEQUENCE 278 AA: 31132 MW: BDB9E08E65D2F92D CRC64;
Query Match 4.5%; Score 14; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 194 AIQMVSEARFKYI 207
Db 190 AIQMVSEARFKYI 203
RESULT 5
RIP2_BRYDI STANDARD: PRT: 282 AA.
AC P98184; Q9580;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN BRYODIN II PRECURSOR (rRNA N-
glycosidase) (EC 3.2.2.22) (BD2).
Bryonia dioica (Red Bryonia).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
NCBI_Taxid:3652;
RN [1]
SEQUENCE FROM N.A.
Siegal C.B., Gawlak S.L., Marquardt II.;
Bryodin 2 a ribosome-inactivating protein isolated from the plant
Bryonia dioica.";
Patent number US5597569, 28-JAN-1997.
[2]

RP SEQUENCE OF 22-42.
RC TISSUE=Root;
RX MEDLINE-95151812: Pubmed-7849072;
RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
Marquardt II.;
"Characterization of ribosome-inactivating proteins isolated from
Bryonia dioica and their utility as carcinoma-reactive
immunoconjugates";
Biochim. Chem. 5:423-429(1994).
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: I34238; -; NOT_ANNOTATED_CDS.
CC HSSP: P09989; LMRJ.
CC InterPro: IPR001574; RIP.
CC Pfam: PF00161; RIP. 1.
CC PRINTS: PR00396; SHIGARICIN.
CC PROSITE: PS00275; SHIGA_RICIN; 1.
CC Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
KW Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
FT ACT_SITE 183 183 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GUCNAC...) (POTENTIAL).
FT SEQUENCE 282 AA: 30754 MW: C52BE2F6A873769C CRC64;
Query Match 3.5%; Score 11; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 VSEARFKYIE 208
Db 181 VSEARFKYIE 191
RESULT 6
RIP2_PHYDI STANDARD: PRT: 32 AA.
AC P34967;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
PROTEIN SYNTHESIS INHIBITOR PD-S2 (RIBOSOME-INACTIVATING PROTEIN
PD-S2) (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
OS Phytolacca dioica (Pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
NCBI_Taxid:29725;
RN [1]
SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE-94032487: Pubmed-8218414;
Parente A., de Luca P., Bolognesi A., Barbieri L., Battelli M.G.,
Abbondanza A., Sande M.J.W., Gigliano G.S., Tazzari P.L., Sirtori F.;
"Purification and partial characterization of single-chain ribosome-
inactivating proteins from the seeds of Phytolacca dioica L.";
Biochim. Biophys. Acta 1216:43-49(1993).
CC -!- FUNCTION: INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS
IMMUNOTOXIN FOR PHARMACOLOGICAL APPLICATIONS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

specific adenosine on the 28S rRNA.
- TISSUE SPECIFICITY: SEEDS.
- PM: GLYCOSYLATED.
- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
PIR: S38528; S38528.
HSP: P10297; LOC.
InterPro: IPR001574; RIP.
Pfam: PF00161; RIP; 1.
PROSITE: PS00275; SHIGA_RICIN; PARTIAL.
Plant defense: Protein synthesis inhibitor; Hydrolase; Glycoprotein;
Toxin.
NON_TER 32 32
SEQUENCE 32 AA: 45BAFEBEE2473CE7 CRC64;
Query Match 3.2%; Score 10; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
45 ESLRQAKDP 54
|||||
21 ESLRQAKDP 30
RESULT 7
IPG_GELMU STANDARD; PRT; 316 AA.
C P33186;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein gelonin precursor. (rRNA N-glycosidase)
(EC 3.2.2.22).
OS Gel.
OC Eukaryota; Viridiplantae; Euphorbiaceae himalaya).
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
OC Eurosids I; Malpighiales; Euphorbiaceae; Gelonium.
NCBI_TaxID=3579;
RN [1]
RP SEQUENCE FROM N.A.
RA Molan P.A., Garrison D.A., Better M.;
RT "Cloning and expression of a gene encoding gelonin, a ribosome-
inactivating protein from Gelonium multiflorum.";
RL Gene 134:223-227(1993).
RN [2]
RP SEQUENCE OF 47-93.
RC TISSUE=Seed;
RX MEDLINE=89326691; PubMed=2753596;
RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
LA Leppl D.;
RT "N-terminal sequence of some ribosome-inactivating proteins.";
RL Int. J. Pept. Protein Res. 33:263-267(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA Hosur M.V., Naik B., Satyamurthy P., Misquith S., Surolia A.,
LA Kannan K.K.;
RT "X-ray structure of gelonin at 1.8-A resolution.";
RL J. Mol. Biol. 250:368-380(1995).
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC - SUBUNIT: HOMODIMER.
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
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CC EMBL: L12243; AAA16312.1;
DR PIR: S16489; S16489.
DR HSP: P09989; IMR3.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PK00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; FALSE_NEG.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KW Glycoprotein.
FT SIGNAL 1 26
FT PROPEP 27 46
FT CHAIN 47 297
FT PROPEP 298 316
FT DISULFD 90 96
FT CARBOHYD 215 235
FT ACT_SITE 212 212
FT CONFLICT 90 90
FT CONFLICT 93 93
SQ SEQUENCE 316 AA: 1252F3E710901B85 CRC64;
Query Match 3.2%; Score 10; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 IOMVSEAAARF 204
|||||
DB 207 IOMVSEAAARF 216
RESULT 8
NIGB_SAMNI STANDARD; PRT; 563 AA.
AC P33183; P33184; P93542;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nigrin b precursor (Agglutinin V) (SNV) [Contains: Nigrin b A chain
(rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;
OC Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Barik;
RX MEDLINE=96215449; PubMed=8647092;
RA Van Damme E.J., Barre A., Roupe P., Van Leuven F., Peumans W.J.;
RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GAINAC-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
RL Eur. J. Biochem. 237:505-513(1996).
RN [2]
RP SEQUENCE OF 26-49 AND 298-321.
RC TISSUE=Barik;
RX MEDLINE=94003077; PubMed=8400135;
RA Gibbs T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
RT "Isolation and partial characterization of nigrin b, a non-toxic
novel type 2 ribosome-inactivating protein from the bark of Sambucus
nigra b.";
RL Plant Mol. Biol. 22:1181-1186(1993).
CC - FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE
B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
ENDOCYTOSIS.
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

specific adenosine on the 28S rRNA.
-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-1- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.

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EMBL: U41299; AAB39475.1;
PIR: S37382; S37382;
PIR: S37383; S37383;
InterPro: IPR001574; RIP;
InterPro: IPR000772; Ricin_B_lectin;
Pfam: PF00161; RIP; 2;
Pfam: PF00652; Ricin_B_lectin; 6;
PRINTS: PR00396; SHICARICIN;
SMART: SM00458; RICIN; 2;
PROSITE: PS00275; SHIGA-RICIN; 1;
PROSITE: PS50231; RICIN_B-LECTIN; 2;
Plant defense: Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
Glycoprotein; Lactin; Signal;
FT SIGNAL 1 25
FT CHAIN 26 297 NIGRIN B A CHAIN.
FT CHAIN 298 563 NIGRIN B B CHAIN.
FT DOMAIN 305 431 RICIN B-TYPE LECTIN 1.
FT DOMAIN 434 559 RICIN B-TYPE LECTIN 2.
FT REPEAT 316 356 1-ALPHA.
FT REPEAT 357 397 1-BETA.
FT REPEAT 400 432 1-GAMMA.
FT REPEAT 445 482 2-ALPHA.
FT REPEAT 486 524 2-BETA.
FT REPEAT 527 554 2-GAMMA.
FT ACT_SITE 188 302 BY SIMILARITY.
FT DISULFID 274 302 INTERCHAIN (BY SIMILARITY).
FT DISULFID 319 338 BY SIMILARITY.
FT DISULFID 360 377 BY SIMILARITY.
FT DISULFID 448 463 BY SIMILARITY.
FT CARBOHYD 489 506 BY SIMILARITY.
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 39 K -> V (IN REF. 2).
SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRC64;

Query Match 3.2%; Score 10; DB 1; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

195 IOMVSEAAEF 204
|||||
183 IOMVSEAAEF 192

RIP1_MOMCH STANDARD; PRT: 286 AA.
RIP1_MOMCH
P16094; P24697;
01-APR-1990 (Rel. 14; Created)
01-MAR-1992 (Rel. 21; Last sequence update)
15-JUN-2002 (Rel. 41; Last annotation update)
Ribosome-inactivating protein momordin I precursor (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-momorcharin) (Alpha-NMC).
Momordica charantia (Bitter melon) (Balsam pear).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids 1: Cucurbitales: Cucurbitaceae: Momordica.
OX NCBI_TaxID=3673;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=91159486; PubMed=2001404;
RA Ho W.K., Liu S.C., Shaw P.C., Young H.W., Ng T.B., Chan W.Y.;
RT "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein.";
RL Biochim. Biophys. Acta 1088:311-314(1991).
RN [2]
RP SEQUENCE OF 24-38.
RC TISSUE=Seed;
RX MEDLINE=89326691; PubMed=2753596;
RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
RA Capri D.;
RT "N-terminal sequence of some ribosome-inactivating proteins.";
RL Int. J. Pept. Protein Res. 33:263-267(1989).
RN [3]
RP SEQUENCE OF 24-70.
RC TISSUE=Seed;
RX MEDLINE=89005108; PubMed=3262509;
RA Casellas P., Bussosoy D., Fatasca A.I., Barbieri L.,
RA Guillemot J.C., Ferrara P., Bolognesi A., Cennini P., Stirpe F.;
RT "Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes kirilowii Maximowicz. Purification, partial characterization and use for preparation of immunotoxins.";
RL Eur. J. Biochem. 176:581-588(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=94356447; PubMed=8075985;
RA Ren J., Wang Y., Dong Y., Stuart D.I.;
RT "The N-glycosidase mechanism of ribosome-inactivating proteins implied by crystal structures of alpha-momorcharin.";
RL Structure 2:7-16(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).
RX MEDLINE=94192822; PubMed=8143869;
RA Hussain J., Tickle I.J., Wood S.P.;
RT "Crystal structure of momordin, a type I ribosome inactivating protein from the seeds of Momordica charantia.";
RL FEBS Lett. 342:154-158(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=93344383; PubMed=7619070;
RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
RT "Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins.";
RL Biochem. J. 309:285-298(1995).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.

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EMBL: X57682; CAA40869.1;
PIR: S14273; RLPUGG;
PIR: S16490; S16490;
PDB: 1AHB; 22-JUN-94.
PDB: 1AHC; 22-JUN-94.
PDB: 1MOM; 31-MAY-94.
PDB: 1MRG; 07-FEB-95.
PDB: 1MRI; 07-FEB-95.
GlycoSuiteDB; P16094;

InterPro: IPR001574; RIP.
 Pfam: PF00161; RIP; 1.
 PRINTS: PR00396; SHIGARICIN.
 PROSITE: PS00275; SHIGA_RICIN; 1.
 Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin; Signal.
 Glycoprotein; 3D-structure.
 SIGNAL 1 23
 CHAIN 24 269 RIBOSOME-INACTIVATING PROTEIN MOMORDIN I.
 PROPEP 270 286 MISSING IN MATURE PROTEIN.
 ACT_SITE 183 183
 CARBOHYD 250 250 N-LINKED (GLCNAC. . .).
 /FTID-CAR-000082.
 SEQUENCE 286 AA: 31532 MW: E1B013ABEBC216CF CRC64:

Query Match 2.9% Score 9; DB 1; Length 286;
 Best Local Similarity 100.0% Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 EAAREFYIE 208
 DB 183 EAAREFYIE 191

RESULT 10

IP22_MOMBA STANDARD: PRT: 286 AA.
 ID RIP2_MOMBA
 IC 29339;
 YT 01-DEC-1992 (Rel. 24, Created)
 YT 01-DEC-1992 (Rel. 24, Last sequence update)
 YT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein momordin II precursor (rRNA
 N-glycosidase) (EC 3.2.2.22).
 YE Momordica balsamina (Bitter melon) (Balsam pear).
 XK Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 XK Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 XK Eucosids I; Cucurbitales; Cucurbitaceae; Momordica.
 NCBI_TaxID-3672;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed.
 RX MEDLINE-93027170; PubMed-1408771;
 RA Ortizgo M., Better M.;
 RA "Momordin II, a ribosome inactivating protein from Momordica
 balsamina, is homologous to other plant proteins."
 RL Nucleic Acids Res. 20:4662-4662(1992).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

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EMBL: Z1175; CAA78166.1;
 PIR: S25360; S25360.
 HSP: P09989; LMRJ.

InterPro: IPR001574; RIP.
 Pfam: PF00161; RIP; 1.

PRINTS: PR00396; SHIGARICIN.
 PROSITE: PS00275; SHIGA_RICIN; 1.

Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin; Signal.
 SIGNAL 1 23
 CHAIN 24 286 RIBOSOME-INACTIVATING PROTEIN MOMORDIN
 II.

ACT_SITE 181 181 BY SIMILARITY

SEQUENCE 286 AA: 32031 MW: 3889FFIAE6B5986 CRC64:

Query Match

2.9% Score 9; DB 1; Length 286;

Best Local Similarity 100.0% Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 EAAREFYIE 208
 DB 181 EAAREFYIE 189

RESULT 11

FAT1_RHIME STANDARD: PRT: 272 AA.
 ID FAT1_RHIME
 IC P58380;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enoyl-[acyl-carrier-protein] reductase [NADH] 1 (EC 1.3.1.9) (NADH-
 dependent enoyl-ACP reductase 1).
 GN FAB1 OR R00898 OR SMC00005.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 NCBI_TaxID-382;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021;
 RX MEDLINE-21396507; PubMed-11481430;
 RA Capela D., Barloy-Hubier F., Gouzy J., Bothie G., Ampe F., Batut J.,
 Boistard P., Becker A., Boutry M., Cadieu F., Dreano S., Gloux S.,
 Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
 Pohl T., Portetelle D., Puehler A., Purcell B., Ramsperger U.,
 Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-
 2,3-dehydroacyl-[acyl-carrier protein] + NADH.
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (by similarity).
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
 DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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 or send an email to license@isb-sib.ch).

EMBL: AL501785; CAC45470.1;
 InterPro: IPR002198; AduI_short.
 Pfam: PF00106; AduI_short; 1.

Oxidoreductase; NAD; Fatty acid biosynthesis; Inner membrane;
 Complete proteome.

NP_BIND 14 40 NAD (BY SIMILARITY)
 SEQUENCE 272 AA: 29148 MW: 1E0FAL8A22CDBE36 CRC64;

Query Match 2.5% Score 8; DB 1; Length 272;
 Best Local Similarity 100.0% Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 LEEKWGI 235
 DB 82 LEEKWGI 89

RESULT 12

PFDA_THEVO STANDARD: PRT: 130 AA.
 ID PFDA_THEVO
 AC Q97BC5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DT

Prefoldin alpha subunit (GimC alpha subunit).
PFDA OR TV0531 OR TV05052388.
Thermoplasma volcanium.
Archaea: Euryarchaeota; Thermoplasma; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=50339;
(1)
SEQUENCE FROM N.A.
RP STRAIN=CSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,
"Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium."
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
CC -!- FUNCTION: Molecular chaperone capable of stabilizing a range of
proteins. Seems to fulfill an ATP-independent, Hsp70-like function
in archaeal de novo protein folding (By similarity).
CC -!- SUBUNIT: Heterohexamer of two alpha and four beta subunits (By
similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PREFOLDIN ALPHA SUBUNIT FAMILY.
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EMBL: AP000992; BAB59673.1;
InterPro: IPR004127; DUF232.
Pfam: PF02996; DUF232; 1.
Chaperone, Complete proteome.
SEQUENCE 130 AA; 14617 MW; 6542126CDCAFA1ED CRC64:
Query Match 2.2%: Score 7; DB 1; Length 130;
Best Local Similarity 100.0%: Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 166 IQLSSD 172
DB 37 IQLSSD 43
RESULT 13
TVA3_MOUSE STANDARD: PRT: 132 AA.
AC P06323;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
KW T-cell receptor alpha chain v region CTL-f3 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
(1)
SEQUENCE FROM N.A.
RX MEDLINE=87053852; PubMed=3409068;
RA Chou H.S., Behlke M.A., Godambe S.A., Russell J.H., Brooks C.G.,
Loh D.Y.;
"T cell receptor genes in an allelically diverse CTL clone: implications for
rearrangement and germ-line diversity of variable gene segments.";
EMBO J. 5:2149-2155(1986).
PIR: A02014; RWSA3.
InterPro: IPR003599; Ig.
Pfam: PF00047; Ig_1.
SMART: SM00409; Ig_1.
T-cell: Receptor; Glycoprotein; Signal.

FT SIGNAL 1 22
FT CHAIN 23 132
FT T-CELL RECEPTOR ALPHA CHAIN V REGION (CTL-
F3).
FT V SEGMENT.
FT DOMAIN 23 114
FT J SEGMENT.
FT CARBOHYD 115 132
FT DISULFID 43 43
FT NON_TER 44 111
FT SEQUENCE 132 AA; 14747 MW; 4E7DC80D7FEDAA67 CRC64:
Query Match 2.2%: Score 7; DB 1; Length 132;
Best Local Similarity 100.0%: Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 88 LMLRRN 94
DB 15 LMLRRN 21
RESULT 14
YURA_MYXXA STANDARD: PRT: 258 AA.
AC P25970;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase in URAA 5' region (EC 1.-.-.) (Fragment).
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
(1)
RN SEQUENCE FROM N.A.
RP STRAIN=DK1622;
RX MEDLINE=92112814; PubMed=1730672;
RA Kimsey H.H., Kaiser D.;
"The orotidine-5'-monophosphate decarboxylase gene of Myxococcus
xanthus. Comparison to the GMP decarboxylase gene family.";
J. Biol. Chem. 267:819-824(1992).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
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EMBL: M79325; NOT_ANNOTATED_CDS.
InterPro: IPR002198; ADH_short.
Pfam: PF0106; adh_short; 1.
PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein: Oxidoreductase.
FT NON_TER 1 1
FT NP_BIND 7 30 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
FT SEQUENCE 258 AA; 27367 MW; 7DB81229D3FE8BF CRC64:
Query Match 2.2%: Score 7; DB 1; Length 258;
Best Local Similarity 100.0%: Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 TFMESLR 48
DB 169 TFMESLR 175
RESULT 15
FA9_RABIT STANDARD: PRT: 275 AA.
AC P16292;

01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor IX (EC 3.4.21.22) (Christmas factor) (Fragment).
F9.
Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90152675; PubMed=2303254;
RA Sarkar G., Koerber D.D., Sommer S.S.;
RT "Direct sequencing of the activation peptide and the catalytic domain
of the factor IX gene in six species.";
RL Genomics 6:131-143(1990).
CC -!- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT
CC PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY
CC CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
CC IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.
CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -!- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE
CC ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2
CC CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
EMBL: M26234; AAA31251.1; -
DSSP: P16293; IPFX.
DR MEROPS: S01.214; -
UR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR00294; VILK_dep_GLA.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00020; tryp_SPC; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; PARTIAL.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Serine protease; Calcium-binding;
KW Hydrolase; Glycoprotein.
FT NON_TER 1
FT ACT_SITE 89 89 CHARGE RELAY SYSTEM.
FT ACT_SITE 137 137 CHARGE RELAY SYSTEM.
FT ACT_SITE 233 233 CHARGE RELAY SYSTEM.
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 275 275
SS SEQUENCE 275 AA: 30776 MW: FE364489AC76BE87 CRC64;
Query Match 2.2% Score 7; DB 1; Length 275;
Best Local Similarity 100.0%; Pred. NO. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
34 NATINKY 40
1111111
128 NATINKY 134

Search completed: May 28, 2003, 10:10:15
Job time : 26 secs

Printed 11/17/2004

GenCore version 5.1.4_p5_4578
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On protein - protein search, using sw model

Run on: May 28, 2003, 10:05:30 ; Search time 85 Seconds
(without alignments)
761.162 Million cell updates/sec

Title: US-09-978-274A-2
Perfect score: 314
Sequence: 1 MKVNLVVVVTLIAWLIAPT.....VLIISTYNNMNLCLFEGF 314

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_ROOTENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rank	Score	Query Match	Length	DB ID	Description
1	314	100.0	314	10 P93444	P93444 phytolacca
2	124	39.5	262	10 Q8S946	Q8S946 phytolacca
3	30	9.6	237	10 Q9ATB3	Q9ATB3 phytolacca
4	28	8.9	261	10 Q8S947	Q8S947 phytolacca
5	21	6.7	313	10 Q941G8	Q941G8 phytolacca
6	21	6.7	339	10 Q8RYA4	Q8RYA4 phytolacca
7	19	6.1	315	10 Q9XFF8	Q9XFF8 phytolacca
8	14	4.5	305	10 Q8W4U4	Q8W4U4 bougainvill
9	11	3.5	136	10 Q8RY69	Q8RY69 gynostemma
10	10	3.2	258	10 Q9S9E4	Q9S9E4 gellonium mu
11	10	3.2	563	10 Q04367	Q04367 sambucus ni
12	10	3.2	563	10 Q945S2	Q945S2 sambucus ni
13	10	3.2	565	10 Q04071	Q04071 sambucus ni
14	10	3.2	566	10 Q04072	Q04072 sambucus ni
15	10	3.2	569	10 P93543	P93543 sambucus ni
16	10	3.2	570	10 Q22415	Q22415 sambucus ni

17	10	3.2	570	10 Q41358	Q41358 sambucus ni
18	10	3.2	592	10 Q8W2E7	Q8W2E7 iris hollan
19	10	3.2	603	10 Q9M053	Q9M053 polygonatum
20	10	3.2	604	10 Q9M654	Q9M654 polygonatum
21	9	2.9	264	10 Q9FSH2	Q9FSH2 monardella c
22	9	2.9	270	10 Q9SA05	Q9SA05 amarantus
23	9	2.9	279	10 Q927Z5	Q927Z5 amarantus
24	9	2.9	286	10 Q9FUV7	Q9FUV7 monardella c
25	9	2.9	293	10 Q8VYU0	Q8VYU0 fatiophya cu
26	9	2.9	294	10 Q93Y66	Q93Y66 dianthus ch
27	9	2.9	294	10 Q93Y65	Q93Y65 dianthus ch
28	9	2.9	294	10 Q93Y64	Q93Y64 dianthus ch
29	8	2.5	242	12 Q80897	Q80897 human papil
30	8	2.5	279	10 Q9MSK6	Q9MSK6 chenopodium
31	8	2.5	279	10 Q9AU63	Q9AU63 chenopodium
32	8	2.5	302	10 P93077	P93077 ceterodendru
33	8	2.5	321	5 Q17149	Q17149 caenorhabdi
34	8	2.5	327	5 Q17150	Q17150 caenorhabdi
35	8	2.5	371	16 Q07018	Q07018 bacillus su
36	8	2.5	458	16 Q92730	Q92730 chlamydia p
37	8	2.5	588	5 P92010	P92010 caenorhabdi
38	8	2.5	953	2 Q85299	Q85299 haemophilus
39	8	2.5	1539	10 Q9LZ75	Q9LZ75 arabidopsis
40	7	2.2	57	2 Q9Z3V1	Q9Z3V1 rhodospirido
41	7	2.2	68	17 Q97XV0	Q97XV0 sulfolobus
42	7	2.2	76	17 Q9RHU3	Q9RHU3 halobacteri
43	7	2.2	88	10 Q8S2B1	Q8S2B1 oryza sativ
44	7	2.2	92	8 Q01307	Q01307 petunia hyb
45	7	2.2	123	3 Q07355	Q07355 saccharomyc

ALIGNMENTS

RESULT 1

P93444	PRELIMINARY:	PRT:	314 AA.
ID	P93444		
AC	P93444		
DT	01-MAY-1997 (TRENBLREL. 03, Created)		
DT	01-MAY-1997 (TRENBLREL. 03, Last sequence update)		
DT	01-MAY-2002 (TRENBLREL. 20, Last annotation update)		
DE	rRNA -glycosidase precursor (EC 3.2.2.22).		
GN	PAP-S		
OS	Phytolacca americana (Common pokeweed).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Caryophyllales; Caryophyllaceae; Phytolaccaceae; Phytolacca.		
OX	NCBI_TaxID=3527;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=SEED;		
RX	MEDLINE=97263479; PubMed=9109394;		
RA	Poyet J., Hoeweler A.;		
RT	*cDNA cloning of the gene encoding the Antiviral Protein from the		
RT	seeds of Phytolacca americana and its expression in E.coli.;		
RL	FEMS Lett. 408:97-100(1997).		
CC	!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE		
CC	SPECIFIC ADENOSINE ON THE 2BS RNA.		
CC	!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.		
DR	EMBL: X98079; CAA66702.1; -		
DR	ISSP: 003464; JAPA.		
DR	InterPro: IPR001574; RIP.		
DR	Tram: PF00161; RIP: 1.		
DR	PRINTS: PR003356; SHICARTICIN.		
DR	PROSITE: PS00275; SHIGA-RICIN: 1.		
KW	Hydrolase; Signal; Toxin.		
FT	SIGNAL		POTENTIAL..
FT	CHAIN	25	314 POTENTIAL..
SQ	SEQUENCE	314 AA:	35323 MW: A89E3CE57789FF9E CMC64;

Query Match: 100.0%; Score: 314; DB: 10; Length: 314;
Best Local Similarity: 100.0%; Pred. No.: 0;
Matches: 314; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

09978274

1 MKVNLVVVTLIAHLIAAPTSTCAINTITDAGNATINKYATFMSLRNQAOKPKLKYC 60
1 MKVNLVVVTLIAHLIAAPTSTCAINTITDAGNATINKYATFMSLRNQAOKPKLKYC 60
61 IPMLPOTNSTPKVLLKQGANLKTITLMLRRNNLYVMGSDPFGNKKRYHFNIDTST 120
61 IPMLPOTNSTPKVLLKQGANLKTITLMLRRNNLYVMGSDPFGNKKRYHFNIDTST 120
121 ERTDVENTICSSSSSRVAMISINSLYPTWTKKAEVNRNOVOLGTOILSSDGIKISGVD 180
121 ERTDVENTICSSSSSRVAMISINSLYPTWTKKAEVNRNOVOLGTOILSSDGIKISGVD 180
181 SPVKTEAFELLLVAIQMVSEAAARFKYIENOVKTNFRAFPDPKVINLEEKWKGISEAIIH 240
181 SPVKTEAFELLLVAIQMVSEAAARFKYIENOVKTNFRAFPDPKVINLEEKWKGISEAIIH 240
241 NAKNGALPKLELVDAKGTWIVLRVDEINRVALLYVNGTCOTTYQNAVFQVLIISTY 300
241 NAKNGALPKLELVDAKGTWIVLRVDEINRVALLYVNGTCOTTYQNAVFQVLIISTY 300
301 YNYMSNLGDLFEFG 314
301 YNYMSNLGDLFEFG 314

RESULT 2

Q8S946 PRELIMINARY; PRT: 262 AA.
AC Q8S946;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DE RNA -glycosidase (EC 3.2.2.22) (Fragment).
GN PAPS2.
OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN (1)
RP SEQUENCE FROM N.A.
RA Honjo E., Watanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB071855; BAB86350.1;
FT NON_TER 1
FT NON_TER 262
SQ SEQUENCE 262 AA; 29486 MW; AF2D010A73C9D18B CRC64;
Query Match 39.5%; Score 124; DB 10; Length 262;
Best Local Similarity 100.0%; Pred. No. 3.6e-125; Mismatches 0; Indels 0; Gaps 0;
Matches 124; Conservative 0;

161 QVQLGQILSSDGIKISGVDSPVKTEAFELLLVAIQMVSEAAARFKYIENOVKTNFRAFY 220
137 QVQLGQILSSDGIKISGVDSPVKTEAFELLLVAIQMVSEAAARFKYIENOVKTNFRAFY 156
221 PDKPVINLEEKWKGISEAIIHNAKNGALPKLELVDAKGTWIVLRVDEINRVALLYVYN 280
197 PDKPVINLEEKWKGISEAIIHNAKNGALPKLELVDAKGTWIVLRVDEINRVALLYVYN 256
281 GTCC 284
257 GTCC 260

RESULT 3

Q8ATN3 PRELIMINARY; PRT: 237 AA.
Q8ATN3;
Q8ATN3;

01-JUN-2001 (TRENBLrel. 17, Created)
01-JUN-2001 (TRENBLrel. 17, Last sequence update)
01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE RNA -glycosidase (EC 3.2.2.22) (Fragment).
GN MPAP.
OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN (1)
RP SEQUENCE FROM N.A.
RA Chen D., Wang X., Zhou G.;
RT "Pokeweed antiviral protein gene, partial cds."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF338910; AAK21951.1;
DR HSSP: P10297; LOCC
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 26534 MW; FE4ADCEE03464783 CRC64;
Query Match 9.6%; Score 30; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.1e-23; Mismatches 0; Indels 0; Gaps 0;
Matches 30; Conservative 0;

QY 190 FLVVAIQMVSEAAARFKYIENOVKTNFRAFY 219
DB 166 FLVVAIQMVSEAAARFKYIENOVKTNFRAFY 195

RESULT 4

Q8S947 PRELIMINARY; PRT: 261 AA.
AC Q8S947;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DE PAP-S1 (Fragment).
GN PAPS1.
OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN (1)
RP SEQUENCE FROM N.A.
RA Honjo E., Watanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB071854; BAB86349.1;
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 29199 MW; D88B998BEFE1F989 CRC64;
Query Match 8.9%; Score 28; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e-21; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0;

QY 190 FLVVAIQMVSEAAARFKYIENOVKTNFRAFY 217
DB 165 FLVVAIQMVSEAAARFKYIENOVKTNFRAFY 192


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06/02/2003
us-09-978-274a-2.oli.rspt
Page 4

RESULT 11
004367 PRELIMINARY: PRT: 503 AA.
ID 004367
AC 004367
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE RNA -glycosidase precursor (EC 3.2.2.22)
OS Sambucus nigra (European elder)
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Asteridae: euasterids II: Dipsacales: Adoxaceae: Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Burle A., Kouge P., Van Leuven F.,
RA Peumans W.J.;
RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
RL derived from a truncated type 2 ribosome-inactivating protein.";
CC Plant J. 12:1251-1260(1997)
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: U76524; AAC15886.1;
DR HSSP: P02879; 2AAL
DR InterPro: IPR000772; R1cin_B_lectin.
DR Pfam: PF00652; R1cin_B_lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 298 563
SQ SEQUENCE 563 AA: 62336 MW: 3E02B6C08E796205 CRC64:
Query Match 3.2%; Score 10; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 IQMVSEAAARF 204
DB 183 IQMVSEAAARF 192

RESULT 12
094552 PRELIMINARY: PRT: 563 AA.
ID 094552
AC 094552
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE RNA -glycosidase (EC 3.2.2.22)
OS Sambucus nigra (European elder)
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Asteridae: euasterids II: Dipsacales: Adoxaceae: Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LEAF;
RA Van Damme E.J.M.;
RT "Characterization and cloning of lectins and ribosome-inactivating
RL proteins from Sambucus nigra leaves.";
CC Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
DR EMBL: U76524; AAC15886.1;
DR HSSP: P02879; 2AAL
DR InterPro: IPR000772; R1cin_B_lectin.
DR Pfam: PF00652; R1cin_B_lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 298 563
SQ SEQUENCE 563 AA: 62336 MW: 3E02B6C08E796205 CRC64:
Query Match 3.2%; Score 10; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 IQMVSEAAARF 204
DB 183 IQMVSEAAARF 192

RESULT 13
094552 PRELIMINARY: PRT: 563 AA.
ID 094552
AC 094552
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE RNA -glycosidase (EC 3.2.2.22)
OS Sambucus nigra (European elder)
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Asteridae: euasterids II: Dipsacales: Adoxaceae: Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LEAF;
RA Van Damme E.J.M.;
RT "Characterization and cloning of lectins and ribosome-inactivating
RL proteins from Sambucus nigra leaves.";
CC Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
DR EMBL: U76524; AAC15886.1;
DR HSSP: P02879; 2AAL
DR InterPro: IPR000772; R1cin_B_lectin.
DR Pfam: PF00652; R1cin_B_lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 298 563
SQ SEQUENCE 563 AA: 62336 MW: 3E02B6C08E796205 CRC64:
Query Match 3.2%; Score 10; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 IQMVSEAAARF 204
DB 183 IQMVSEAAARF 192
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CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.

DE EMBL: AF409135; AAL04123.1; ..

DR InterPro: IPR000772; Ricin_B_lectin.

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE rRNA -glycosidase precursor (EC 3.2.2.22).

DR Pfam: PF00161; RIP; 1.

DR PROSITE: PS00331; RICIN_B_LFECTIN; 2.

DR PROSITE: PS00375; SHIGA_RICIN; UNKNOWN_1.

KW Hydrolase; Toxin.

QY SEQUENCE 563 AA: 62242 MW: 077CBEDCF33BF10 CRC64:

Query Match 3.2%: Score 10; DB 10; Length 563;

Best Local Similarity 100.0%; Pred. No. 0.094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 IQMVSEAAAF 204

|||||

DB 183 IQMVSEAAAF 192

RESULT 13

Q04071

AC Q04071 PRELIMINARY: PRT: 565 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE rRNA -glycosidase precursor (EC 3.2.2.22).

OS Sambucus nigra (European elder).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.

KW NCBI_TaxID=4202;

QY SEQUENCE FROM N.A.

RE MEDLINE-97236787; PubMed-9079659;

RR Van Damme E.J.M., Barre A., Rouge P., Van Leuven F., Peumans W.J.;

RT Isolation and molecular cloning of a novel type 2 ribosome-

RT inactivating protein with an inactive B chain from elderberry

RT (Sambucus nigra) bark.;

RL J. Biol. Chem. 272:8353-8360(1997).

CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.

CC EMBL: U58357; AAC49672.1; ..

DR HSSP: P02879; 2A1.

DR InterPro: IPR000772; Ricin_B_lectin.

DR Pfam: PF00652; Ricin_B_lectin; 6.

DR PRINTS: PR00161; RIP; 1.

DR SMART: SM00458; SHIGARICIN.

DR PROSITE: PS00331; RICIN_B_LFECTIN; 2.

DR PROSITE: PS00275; SHIGA_RICIN; 1.

KW Hydrolase; Signal; Toxin.

QY SEQUENCE 565 AA: 62348 MW: CD774CCU2593A26 CRC64:

Query Match 3.2%: Score 10; DB 10; Length 565;

Best Local Similarity 100.0%; Pred. No. 0.094;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 IQMVSEAAAF 204

|||||

DB 188 IQMVSEAAAF 197

RESULT 14

Q04072

AC Q04072 PRELIMINARY: PRT: 566 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE rRNA -glycosidase precursor (EC 3.2.2.22).

OS Sambucus nigra (European elder).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.

KW NCBI_TaxID=4202;

QY SEQUENCE FROM N.A. AND SEQUENCE OF 29-38 AND 304-309.

RE TISSUE-BARK;

RR Van Damme E.J.M., Roy S., Barre A., Gitores L., Mostafapour K.,

RT Rouge P., Van Leuven F., Girdes T., Goldstein I.J., Peumans W.J.;

RT "Elderberry (Sambucus nigra) bark contains two structurally different

RT Neu5Ac(alpha2,6)Gal/GalNAc-binding type 2 ribosome-inactivating

RT proteins.;"

Cur. J. Biochem. 245:648-655(1997).
-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS. THIS IS ACHIEVED THROUGH THE CATALYTIC INACTIVATION OF
60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF
28 S RNA (BY SIMILARITY).
-!- FUNCTION: THE B CHAIN IS RESPONSIBLE FOR CELL AGGLUTINATION
(LECTIN ACTIVITY). AGGLUTINATION IS INHIBITED BY
NEUSAC(APH2,6) LACTOSE, AND N-LINKED GLYCOPROTEINS SUCH AS FETUIN
AND OROSOMUCOID (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANT RIBOSOME-INACTIVATING
PROTEINS. BELONGS TO TYPE 2 RIP.
EMBL: U66191; AAC49754.1; --
HSSP: P02879; 2AA1.
InterPro: IPR000772; Ricin_B_lectin.
InterPro: IPR001574; RIP.
Pfam: PF00652; Ricin_B_lectin; 6;
DR PFam: PF00161; RIP; 1;
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2;
DR PROSITE: PS00231; RICIN_B_LECTIN; 2;
DR PROSITE: PS00275; SHIGA_RICIN; 1;
KW Signal: Hydrolase; Glycosidase; Toxin; Glycoprotein; Lectin.
FT SIGNAL 1 28
FT CHAIN 29 291 RIBOSOME-INACTIVATING PROTEIN SNAI', A
FT CHAIN 292 303 LINKER PEPTIDE.
FT CHAIN 304 569 RIBOSOME-INACTIVATING PROTEIN SNAI', B
FT CHAIN 304 569 CHAIN.
FT REPEAT 325 372 1-ALPHA.
FT REPEAT 366 401 1-BETA.
FT REPEAT 404 436 1-GAMMA.
FT REPEAT 448 488 2-ALPHA.
FT REPEAT 492 530 2-BETA.
FT REPEAT 533 566 2-GAMMA.
FT ACT_SITE 201 201 BY SIMILARITY.
FT DISULFID 286 311 INTERCHAIN (BY SIMILARITY).
FT DISULFID 328 347 BY SIMILARITY.
FT DISULFID 369 381 BY SIMILARITY.
FT DISULFID 451 466 BY SIMILARITY.
FT DISULFID 495 512 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC...), (POTENTIAL).
SQ SEQUENCE 569 AA; 62598 MW; 82B9C89A3E1F9AD CRC64;

Query Match 3.2% Score 10; DB 10; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 IQMVSEARF 204

DE 196 IQMVSEARF 205

Search completed: May 28, 2003, 10:11:48
Jelly time : 87 secs

GenCore version 5.1.4.p5.4578
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protein - protein search, using sw model

run on: May 28, 2003, 10:08:25 ; Search time 29 Seconds
(without alignments)
318.579 Million cell updates/sec

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perfect score: 314

sequence: 1 MKVNLVVVTLIAWLAAPT.....VIISTYYNMSNLGLDFEGF 314

scoring table: OLIGO
Gapop 60.0, Gapext 60.0

searched: 262574 seqs, 29422922 residues

word size: 0

total number of hits satisfying chosen parameters: 262574

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Listing first 45 summaries

database:

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	30	9.6	313	1	US-08-373-858-2
2	30	9.6	313	1	US-08-500-611-2
3	30	9.6	313	2	US-08-500-694-2
4	30	9.6	313	4	US-09-005-273-2
5	30	9.6	313	4	US-09-005-273-4
6	30	9.6	313	4	US-08-501-253A-2
7	30	9.6	313	5	PCT-US96-11546-2
8	28	8.9	261	1	US-07-901-707-9
9	28	8.9	261	1	US-07-988-430-9
10	28	8.9	261	1	US-08-435-336-9
11	28	8.9	261	1	US-08-378-761A-79
12	28	8.9	261	1	US-08-485-286-79
13	28	8.9	261	1	US-08-488-1138-9
14	28	8.9	261	1	US-08-477-4848-9
15	28	8.9	261	2	US-08-646-360-9
16	28	8.9	261	4	US-08-839-765-9
17	28	8.9	261	4	US-09-136-389-9
18	28	8.9	261	4	US-09-610-838-9
19	28	8.9	261	5	PCT-US92-09487-9
20	26	8.3	48	4	US-08-776-059-20
21	26	8.3	48	4	US-08-776-059-21
22	26	8.3	48	4	US-08-776-059-22
23	21	6.7	21	4	US-08-776-059-27
24	19	6.1	305	1	US-08-138-636-2
25	19	6.1	305	1	US-08-319-622A-2
26	19	6.1	305	1	US-08-471-564-2
27	14	4.5	21	4	US-08-776-059-25

28	14	4.5	47	4	US-08-776-059-15	Sequence 15, Appl
29	14	4.5	250	1	US-07-854-8458-8	Sequence 8, Appl
30	14	4.5	250	1	US-07-901-707-8	Sequence 8, Appl
31	14	4.5	250	1	US-07-988-430-8	Sequence 8, Appl
32	14	4.5	250	1	US-08-425-336-8	Sequence 8, Appl
33	14	4.5	250	1	US-08-378-761A-76	Sequence 76, Appl
34	14	4.5	250	1	US-08-485-286-76	Sequence 76, Appl
35	14	4.5	250	1	US-08-488-1138-8	Sequence 8, Appl
36	14	4.5	250	1	US-08-477-4848-8	Sequence 8, Appl
37	14	4.5	250	2	US-08-646-360-8	Sequence 8, Appl
38	14	4.5	250	4	US-08-839-765-8	Sequence 8, Appl
39	14	4.5	250	4	US-09-136-389-8	Sequence 8, Appl
40	14	4.5	250	4	US-09-610-838-8	Sequence 8, Appl
41	14	4.5	250	5	PCT-US92-09487-8	Sequence 8, Appl
42	21	3.5	32	1	US-08-324-301-4	Sequence 4, Appl
43	11	3.5	282	1	US-08-324-301-15	Sequence 15, Appl
44	10	3.2	251	1	US-07-901-707-2	Sequence 2, Appl
45	10	3.2	251	1	US-07-988-430-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1.

US-08-373-858-2
; Sequence 2, Application US/08373858

; Patent No. 5633155

; GENERAL INFORMATION:

; APPLICANT: Kim, Man-Keun

; APPLICANT: Lee, Kwan-Ilo

; APPLICANT: Na, Byoung-Kook

; APPLICANT: Jeoung, Han-Seung

; APPLICANT: Choi, Kyu-Whan

; APPLICANT: Moon, Young-Ho

; APPLICANT: Jeon, Hong-Seob

; TITLE OF INVENTION: Expression Vector for Phytolacca

; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Darby & Darby

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: US

; ZIP: 10022-7513

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/373,858

; FILING DATE: 18-JAN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Peter

; REGISTRATION NUMBER: 25,351

; REFERENCE/DOCKET NUMBER: 0136/17986-US1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7770

; TELEFAX: 212-753-6237

; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 313 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Phytolacca americana

REGISTRATION NUMBER: 33-071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-273-2

Query Match 9.6% Score 30; DB 4; Length 313;
Best Local Similarity 100.0% Pred. No. 4.9e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 190 FLVATQMVSEAAAEKFIENQVKTENRAF 219
Db 188 FLVATQMVSEAAAEKFIENQVKTENRAF 217

RESULT 5
JS-09-005-273-4
Sequence 4, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESSEE: MENTLIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33-071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-273-4

Query Match 9.6% Score 30; DB 4; Length 313;

Best Local Similarity 100.0% Pred. No. 4.9e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 190 FLVATQMVSEAAAEKFIENQVKTENRAF 219
Db 188 FLVATQMVSEAAAEKFIENQVKTENRAF 217

RESULT 6
US-08-501-253A-2
Sequence 2, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckird, Fatih
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 50 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-501-253A-2

Query Match 9.6% Score 30; DB 4; Length 313;
Best Local Similarity 100.0% Pred. No. 4.9e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 190 FLVATQMVSEAAAEKFIENQVKTENRAF 219
Db 188 FLVATQMVSEAAAEKFIENQVKTENRAF 217

RESULT 7
PCT-US96-11546-2
Sequence 2, Application PCT/US9611546
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: HNAS Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Roley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-11546-2

Query Match 9.6% Score 30; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 4.9e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 190 FLVVAIQMVSEAAAEKFIENQVKTNFNR 219
D 188 FLVVAIQMVSEAAAEKFIENQVKTNFNR 217
RESULT 8
US-07-901-707-9
Sequence 9, Application US/07901707
Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
COMPOSITION AND USE FOR RIBOSOME-INACTIVATING PROTEINS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 27129/30910

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-9

Query Match 8.9% Score 28; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 FLVVAIQMVSEAAAEKFIENQVKTNFNR 217
D 165 FLVVAIQMVSEAAAEKFIENQVKTNFNR 192

RESULT 9
US-07-988-430-9
Sequence 9, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
PREPARATION AND USE FOR RIBOSOME-INACTIVATING PROTEINS
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-9

Query Match 8.9% Score 28: DB 1: Length 261:

Best Local Similarity 100.0% Pred. No. 3.5e-19:

Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 190 FLVATQMVSEARFKYIENQVKTNFR 217

Db 165 FLVATQMVSEARFKYIENQVKTNFR 192

RESULT 10

US-08-425-336-9

Sequence 9, Application US/08425336

Patent No. 5621083

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studolka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Thomas C.

REGISTRATION NUMBER: P-36,989

REFERENCE/DOCKET NUMBER: 31394

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-425-336-9

Query Match

Best Local Similarity 100.0% Pred. No. 3.5e-19:

Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 190 FLVATQMVSEARFKYIENQVKTNFR 217

Db 165 FLVATQMVSEARFKYIENQVKTNFR 192

RESULT 11

US-08-378-761A-79

Sequence 79, Application US/08378761A

Patent No. 5635384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDREA T. BORUCKI

STREET: 9330 ZIONSVILLE ROAD

CITY: INDIANAPOLIS

STATE: IN

COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,761A

FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BORUCKI, ANDREA T

REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 337-4846

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-761A-79

Query Match

Best Local Similarity 100.0% Score 28: DB 1: Length 261:

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 190 FLVATQMVSEARFKYIENQVKTNFR 217

Db 165 FLVATQMVSEARFKYIENQVKTNFR 192

RESULT 12

US-08-485-286-79

Sequence 79, Application US/08485286

Patent No. 5646026

Patent No. 5646026 5646119

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: ANDREA T. BORUCKI

STREET: 9330 ZIONSVILLE ROAD

CITY: INDIANAPOLIS

STATE: IN

COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-9

Query Match 8.9% Score 28; DB 1: Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 FLVAIQMVSEAAAEKYEIENOVKTNFR 217
|||||
Db 165 FLVAIQMVSEAAAEKYEIENOVKTNFR 192

RESULT 15

US-08-646-360-9

Sequence 9, Application US/08646360

Patent No. 5837491

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-9

Query Match 8.9% Score 28; DB 2: Length 261;
Best Local Similarity 100.0%; Pred. No. 3.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 FLVAIQMVSEAAAEKYEIENOVKTNFR 217
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Db 165 FLVAIQMVSEAAAEKYEIENOVKTNFR 192

Search completed: May 28, 2003, 10:13:16
Job time : 30 secs

06/02/2003

1591

Printed 11/17/2004

GenCore version 5.1.4-p5_4578
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protein - protein search, using sw model

Run On: May 28, 2003, 10:11:56 ; Search time 57 Seconds
(Without alignments)
546,320 Million cell updates/sec

Title: US-09-978-274A-2

Perfect score: 314

Sequence: 1 MKVMLVVVVTLIAWIAAPT.....VIISTYYNMSNLGLDFEGF 314

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Gapop 60.0 , Gapext 60.0

Searched: 375593 seqs, 99172665 residues

Word size : 0

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	314	100.0	314	10	US-09-978-274A-2	Sequence 2, Appli
2	262	83.4	263	10	US-09-978-274A-4	Sequence 4, Appli
3	153	48.7	154	10	US-09-978-274A-6	Sequence 6, Appli
4	109	34.7	110	10	US-09-978-274A-8	Sequence 8, Appli
5	14	4.5	250	9	US-09-792-793A-36	Sequence 36, Appli
6	10	3.2	251	10	US-09-765-527-247	Sequence 247, App
7	10	3.2	293	10	US-09-765-527-259	Sequence 259, App
8	10	3.2	309	10	US-09-765-527-253	Sequence 253, App
9	10	3.2	332	10	US-09-765-527-251	Sequence 251, App
10	8	2.5	69	10	US-09-872-523-62	Sequence 62, Appli
11	8	2.5	70	10	US-09-872-523-60	Sequence 60, Appli
12	8	2.5	140	10	US-09-764-864-1447	Sequence 1447, Ap
13	7	2.2	247	10	US-09-765-272-170	Sequence 170, App
14	7	2.2	489	9	US-09-738-626-3805	Sequence 3805, Ap
15	7	2.2	554	9	US-09-878-672-2	Sequence 2, Appli
16	7	2.2	554	10	US-09-800-396-4	Sequence 4, Appli
17	7	2.2	563	9	US-09-878-672-3	Sequence 3, Appli
18	7	2.2	563	9	US-09-769-787-27	Sequence 27, Appli
19	7	2.2	563	9	US-09-769-787-28	Sequence 28, Appli

Printed

20	7	2.2	953	10	US-09-888-615-66	Sequence 66, Appli
21	6	1.9	22	10	US-09-864-761-40447	Sequence 40447, A
22	6	1.9	29	10	US-09-864-761-47020	Sequence 47020, A
23	6	1.9	30	10	US-09-864-761-41595	Sequence 41595, A
24	6	1.9	30	10	US-09-864-761-48395	Sequence 48395, A
25	6	1.9	35	10	US-09-870-893-122	Sequence 122, App
26	6	1.9	35	12	US-10-001-879-197	Sequence 177, App
27	6	1.9	39	10	US-09-864-761-35239	Sequence 35239, A
28	6	1.9	41	10	US-09-864-761-41438	Sequence 41438, A
29	6	1.9	46	10	US-09-864-761-42923	Sequence 42923, A
30	6	1.9	52	10	US-09-864-761-33973	Sequence 33973, A
31	6	1.9	53	10	US-09-864-761-44587	Sequence 44587, A
32	6	1.9	57	12	US-10-001-843-154	Sequence 154, App
33	6	1.9	59	9	US-10-092-154-983	Sequence 983, App
34	6	1.9	59	10	US-09-864-761-46641	Sequence 46641, A
35	6	1.9	59	10	US-09-764-847-983	Sequence 983, App
36	6	1.9	66	9	US-10-277-156-2	Sequence 2, Appli
37	6	1.9	66	10	US-09-867-550-806	Sequence 806, App
38	6	1.9	68	9	US-10-277-156-4	Sequence 4, Appli
39	6	1.9	68	10	US-09-864-761-41886	Sequence 41886, A
40	6	1.9	69	10	US-09-864-761-38641	Sequence 38641, A
41	6	1.9	75	10	US-09-864-761-46336	Sequence 46336, A
42	6	1.9	77	9	US-09-796-692-1417	Sequence 1417, Ap
43	6	1.9	77	9	US-09-796-692-1885	Sequence 1885, Ap
44	6	1.9	77	9	US-10-040-862-1417	Sequence 1417, Ap
45	6	1.9	77	9	US-10-040-862-1885	Sequence 1885, Ap

ALIGNMENTS

RESULT 1
US-09-978-274A-2
; Sequence 2, Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-2

Query Match	100.0%	Score 314	DB 10	Length 314
Best Local Similarity	100.0%	Pred. No. 6.4e-283		
Matches 314	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MKVMLVVVVTLIAWIAAPTSCAINTITFDAGNATINKYATFMESLNQAKDPKLCYVG	60	
DB	1	MKVMLVVVVTLIAWIAAPTSCAINTITFDAGNATINKYATFMESLNQAKDPKLCYVG	60	
QY	61	IMPDPDTNSTPKYLLVKLGANLKTITLMLRRNNLYVNCYSDDPENGKRCRYHIFNDITST	120	
DB	61	IMPDPDTNSTPKYLLVKLGANLKTITLMLRRNNLYVNCYSDDPENGKRCRYHIFNDITST	120	
QY	121	ERTDVENTLCSSSSSRVAMSINYSLSYPTMEKKAFVNSRNQVOIGIQILSSHICKLSWD	180	
DB	121	ERTDVENTLCSSSSSRVAMSINYSLSYPTMEKKAFVNSRNQVOIGIQILSSHICKLSWD	180	
QY	181	SFPVKTEAFFLLVALIQHVSEAAARKYINENKVFYDPKVINLEKWKIISAIIH	240	
DB	181	SFPVKTEAFFLLVALIQHVSEAAARKYINENKVFYDPKVINLEKWKIISAIIH	240	

241 NAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTYONAMESOVLIISTY 300
241 NAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTTYONAMESOVLIISTY 300
301 YNYSMLGDLFEFG 314
301 YNYSMLGDLFEFG 314

RESULT 2

US-09-978-274A-4
; Sequence 4, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-4

Query Match 83.4%; Score 262; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 8.1e-235; Indels 0; Gaps 0;
Matches 262; Conservative 0; Mismatches 0;

QY 25 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLMDPTNSTPKYLLVKKLOGANLK 84
DB 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLMDPTNSTPKYLLVKKLOGANLK 61
QY 85 TITMLRRNNLYVMGYSDFPNCNKCRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 144
DB 62 TITMLRRNNLYVMGYSDFPNCNKCRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 121
QY 145 SLYPTMEKKAEVNSRNOVLGQIQLSSDGIKSGVDSPPVKTAEFFLLVAIQMVSEAAKF 204
DB 122 SLYPTMEKKAEVNSRNOVLGQIQLSSDGIKSGVDSPPVKTAEFFLLVAIQMVSEAAKF 181
QY 205 KYIENQVKTNRNRAFYDPKVINLEEKWKISETAIIHNAKNGALPKLELVDAKGTWIVL 264
DB 182 KYIENQVKTNRNRAFYDPKVINLEEKWKISETAIIHNAKNGALPKLELVDAKGTWIVL 241
QY 265 RVDEINRDVALLKYVNGTCQTT 286
DB 242 RVDEINRDVALLKYVNGTCQTT 263

RESULT 3

US-09-978-274A-6
; Sequence 6, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14

; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-6

Query Match 48.7%; Score 153; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 4.7e-134;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLMDPTNSTPKYLLVKKLOGANLK 84
DB 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLMDPTNSTPKYLLVKKLOGANLK 61
QY 85 TITMLRRNNLYVMGYSDFPNCNKCRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 144
DB 62 TITMLRRNNLYVMGYSDFPNCNKCRYHIFNDITSTERTDVENTLCSSSSSRVAMSINYN 121
QY 145 SLYPTMEKKAEVNSRNOVLGQIQLSSDGIKSGVDSPPVKTAEFFLLVAIQMVSEAAKF 177
DB 122 SLYPTMEKKAEVNSRNOVLGQIQLSSDGIKSGVDSPPVKTAEFFLLVAIQMVSEAAKF 154

RESULT 4

US-09-978-274A-8
; Sequence 8, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-8

Query Match 34.7%; Score 109; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 2e-93;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 178 GVDSPVKTAEFFLLVAIQMVSEAAKFYIENQVKTNRNRAFYDPKVINLEEKWKISET 237
DB 2 GVDSPVKTAEFFLLVAIQMVSEAAKFYIENQVKTNRNRAFYDPKVINLEEKWKISET 61
QY 238 ATHNAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 286
DB 62 ATHNAKNGALPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 110

RESULT 5

US-09-792-793A-36
; Sequence 36, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601b
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 250
TYPE: PRT
ORGANISM: Momordica charantia
US-09-792-793A-36

Query Match 4.5% Score 14; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 194 AIONVSEARF 207
DB 162 AIONVSEARF 175

RESULT 6

US-09-765-527-247
Sequence 247, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 247:

SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-765-527-247

Query Match 3.2% Score 10; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 195 IONVSEARF 204
DB 161 IONVSEARF 170

RESULT 7

US-09-765-527-259
Sequence 259, Application US/09765527

Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259

Query Match 3.2% Score 10; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 195 IONVSEARF 204
DB 183 IONVSEARF 192

RESULT 8

US-09-765-527-253
Sequence 253, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527

09978274

FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-765-527-253

Query Match 3.2%: Score 10; DB 10; Length 309;
Best Local Similarity 100.0%: Pred. No. 0.25; 0: Indels 0: Gaps 0:
Matches 10; Conservative 0; Mismatches 0

QY 195 IQMVSEAAAF 204
|||||
DB 183 IQMVSEAAAF 192

RESULT 9
US-09-765-527-251
Sequence 251, Application US/09765527
Patent No. US2002000638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251

Query Match 3.2%: Score 10; DB 10; Length 332;
Best Local Similarity 100.0%: Pred. No. 0.26; 0: Indels 0: Gaps 0:
Matches 10; Conservative 0; Mismatches 0

QY 195 IQMVSEAAAF 204
|||||
DB 183 IQMVSEAAAF 192

RESULT 10
US-09-872-523-62
Sequence 62, Application US/09872523
Patent No. US20020137906A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Davison, Ewa M.
APPLICANT: Lu, Xiaowei
TITLE OF INVENTION: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
CURRENT APPLICATION NUMBER: US/09/872,523
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,802
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 62
LENGTH: 69
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-872-523-62

Query Match 2.5%: Score 8; DB 10; Length 69;
Best Local Similarity 100.0%: Pred. No. 4.8; 0: Indels 0: Gaps 0:
Matches 8; Conservative 0; Mismatches 0

QY 305 SNLGDLEF 312
|||||
DB 43 SNLGDLEF 50

RESULT 11
US-09-872-523-60
Sequence 60, Application US/09872523
Patent No. US20020137906A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Davison, Ewa M.
APPLICANT: Lu, Xiaowei
TITLE OF INVENTION: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
CURRENT APPLICATION NUMBER: US/09/872,523
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,802
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 70
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-872-523-60

Query Match 2.5%: Score 8; DB 10; Length 70;
Best Local Similarity 100.0%: Pred. No. 4.9; 0: Indels 0: Gaps 0:
Matches 8; Conservative 0; Mismatches 0

QY 305 SNLGDLEF 312
|||||
DB 43 SNLGDLEF 50

RESULT 12

US-09-764-864-1447
Sequence 1447, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764.864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1447
LENGTH: 140
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-864-1447

Query Match 2.3% Score 8; DB 10; Length 140;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Y 17 AAPTSTCA 24
I I I I I I I I
b 16 AAPTSTCA 23

RESULT 13
US-09-765-272-170
Sequence 170, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765.272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961.083
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 170:

SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-09-765-272-170

Query Match 2.2% Score 7; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 252 ELVDAKG 258
I I I I I I I I
DU 139 ELVDAKG 145

RESULT 14
US-09-738-626-3805
Sequence 3805, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAT, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OKAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738.626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 95/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280908
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3805
LENGTH: 489
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3805

Query Match 2.3% Score 7; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 11 LIAWLIA 17
I I I I I I I I
DU 198 LIAWLIA 204

RESULT 15
US-09-878-672-2
Sequence 2, Application US/09878672
Publication No. US20030049812A1
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
TITLE OF INVENTION: NOVEL histidine kinase
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch St
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/878.672
FILING DATE: 11-Jun-2001
CLASSIFICATION: <Unknown>

Mon Jun 2 10:55:00 2003

us-09-978-274a-2.oli.rapb

Page 6

09978274
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,481
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10022-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
JS-09-878-672-2

Query Match 2.2%; Score 7; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 252 ELVDKAG 258
1111111
2b 158 ELVDKAG 164

Search completed: May 28, 2003, 10:21:55
Job time : 58 secs

SRNT

Printed: 11/17/2004

06/02/2003

165

241 GCACCACTAAACCACTTACACTAATGCTGAGACGAATAACTTATACGTGATGGCTAT 300
 241 GCACCACTAAACCACTTACACTAATGCTGAGACGAATAACTTATACGTGATGGCTAT 300
 301 TCTGATCCCTTCAATGCAATAGTGTGCTGATGATATATTAATGATATTTACAGGAC 360
 301 TCTGATCCCTTCAATGCAATAGTGTGCTGATGATATATTAATGATATTTACAGGAC 360
 361 GAACGCACTGATGGGAGATACCTTTTGTGCTCAAGTCTTCTGCTGATGATGCTTAC 420
 361 GAACGCACTGATGGGAGATACCTTTTGTGCTCAAGTCTTCTGCTGATGATGCTTAC 420
 421 ATTAACCTACAATAGCTTATATCCGACCATGAGAAAGAGAGAGAGAGAGAGAGAG 480
 421 ATTAACCTACAATAGCTTATATCCGACCATGAGAAAGAGAGAGAGAGAGAGAGAG 480
 481 CAAGTCCAATTTGGCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 540
 481 CAAGTCCAATTTGGCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCA 540
 541 TCATTCCTCTGAAACCTGAGGCTTTTCTGCTGATGATGATGATGATGATGATGATG 600
 541 TCATTCCTCTGAAACCTGAGGCTTTTCTGCTGATGATGATGATGATGATGATGATG 600
 601 GCAGCGGATTCAGTACATAGAGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 660
 601 GCAGCGGATTCAGTACATAGAGACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 660
 661 CTGATCCCAAGTAAATTAATTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 661 CTGATCCCAAGTAAATTAATTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 721 AATGCCAAGTAAATTTACCAACCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 780
 721 AATGCCAAGTAAATTTACCAACCACTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 780
 781 TGGATGTTCTTGAAGTGAATGAATCAATCGTATGATGATGATGATGATGATGATGATG 840
 781 TGGATGTTCTTGAAGTGAATGAATCAATCGTATGATGATGATGATGATGATGATGATG 840
 841 GGAACCTGTCAGACACTTACCAAAATGCCATGCTCTCAAGTATTAATTTCTACTTAT 900
 841 GGAACCTGTCAGACACTTACCAAAATGCCATGCTCTCAAGTATTAATTTCTACTTAT 900
 901 TATAATTTATGCTTATCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 945
 901 TATAATTTATGCTTATCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 945

RESULT 2
 US-09-978-274A-3
 : Sequence 3, Application US/09978274A
 : Patent No. US20020116737A1

GENERAL INFORMATION:
 : APPLICANT: Thomas, Christopher
 : APPLICANT: McPherson, Michael
 : APPLICANT: Atkinson, Howard
 : APPLICANT: Neelam, Anil
 : TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 : FILE REFERENCE: 9341-028
 : CURRENT APPLICATION NUMBER: US/09/978, 274A
 : CURRENT FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 0025225.4
 : PRIOR FILING DATE: 2000-10-14
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 3
 : LENGTH: 792
 : TYPE: DNA
 : ORGANISM: Phytolacca americana
 : US-09-978-274A-3

Query Match 78.08; Score 737; DB 10; Length 792;
 Best Local Similarity 99.98; Pred. No. 0;
 Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 73 ATAATACGATCACCCTTTGATGCTGAAATGCCACCAATTAACAAATATGACACCTTTATG 132
 DB 4 ATAATACGATCACCCTTTGATGCTGAAATGCCACCAATTAACAAATATGACACCTTTATG 63
 QY 133 GAATCTCTTCTGATTAATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATGCTA 192
 DB 64 GAATCTCTTCTGATTAATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATGCTA 123
 QY 193 CCTGATACCTAATTCGACCCCTTACTTATGCTGTAAGCTTCAAGTCCAAAGTCCAAAGT 252
 DB 124 CCTGATACCTAATTCGACCCCTTACTTATGCTGTAAGCTTCAAGTCCAAAGTCCAAAGT 183
 QY 253 ACCATACACATTAATGCTGAGACCAATTAATGCTGATGCTGCTTATTCGATGCTTCTTC 312
 DB 184 ACCATACACATTAATGCTGAGACCAATTAATGCTGATGCTGCTTATTCGATGCTTCTTC 243
 QY 313 AATGGCAATGCTGCTTACCATATATTTAATGATATTAACAAGCAGGACCAATGCTGAT 372
 DB 244 AATGGCAATGCTGCTTACCATATATTTAATGATATTAACAAGCAGGACCAATGCTGAT 303
 QY 373 GTGAGAAATCTCTTCTGCTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
 DB 304 GTGAGAAATCTCTTCTGCTCAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
 QY 433 AGCTTATATCCGACCATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
 DB 364 AGCTTATATCCGACCATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
 QY 493 GGAATTCAAATCTACGACCTGACATTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
 DB 424 GGAATTCAAATCTACGACCTGACATTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
 QY 553 AATCTGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
 DB 484 AATCTGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
 QY 613 AACTATATAGAGACCAAGTCAAGACTAATTTTATAGAGACTTCTGCTGCTGCTGCTGCTG 672
 DB 544 AACTATATAGAGACCAAGTCAAGACTAATTTTATAGAGACTTCTGCTGCTGCTGCTGCTG 603
 QY 673 GTAATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
 DB 604 GTAATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
 QY 733 GGGGCTTTTACCCCAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 792
 DB 564 GGGGCTTTTACCCCAACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 723
 QY 793 AGAGTGGATGAATCAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 852
 DB 724 AGAGTGGATGAATCAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 783
 QY 853 ACAACTTA 860
 DB 784 ACAACTTA 791

RESULT 3
 US-09-978-274A-19
 : Sequence 19, Application US/09978274A
 : Patent No. US20020116737A1
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Christopher
 : APPLICANT: McPherson, Michael
 : APPLICANT: Atkinson, Howard
 : APPLICANT: Neelam, Anil
 : TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 : FILE REFERENCE: 9341-028
 : CURRENT APPLICATION NUMBER: US/09/978, 274A

Query Match 75.3% Score 712; DB 10; Length 1092;
Best Local Similarity 99.9% Pred. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 73 ATAAATACGATCACCCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 132
DB 4 ATAAATACGATCACCCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 63
QY 133 GAATCTCTTCTGTAATCAACGGAAGATCCAAACTAAATGCTATGCCATACCAATGCTA 192
DB 64 GAATCTCTTCTGTAATCAACGGAAGATCCAAACTAAATGCTATGCCATACCAATGCTA 123
QY 193 CCTGATACCTAATCGACCCCTTAAGTACTTATTGTTAAGCTCCAAAGTCCAAACCTTAAA 252
DB 124 CCTGATACCTAATCGACCCCTTAAGTACTTATTGTTAAGCTCCAAAGTCCAAACCTTAAA 183
QY 253 ACCATACCTAATCGTACGACCAATACTATACGCTGATGGCTATTCTGATCCCTTC 312
DB 184 ACCATACCTAATCGTACGACCAATACTATACGCTGATGGCTATTCTGATCCCTTC 243
QY 313 AATGGCAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
DB 244 AATGGCAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
QY 373 GTGGAGAACTACTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
DB 424 GGAATTCAAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
QY 553 AAACTAGGCTTTTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
DB 484 AAACTAGGCTTTTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 613 AAGTACATAGCAACCACTCAAGCTAATTTTAAATAGACATCTTACCTGATCCCAAA 572
DB 544 AAGTACATAGCAACCACTCAAGCTAATTTTAAATAGACATCTTACCTGATCCCAAA 603
QY 673 GTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 732
DB 604 GTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 563
QY 733 GGGGCTTTACCAACCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
DB 664 GGGGCTTTACCAACCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
QY 793 AGAGTGGATGAATCAATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
DB 724 AGAGTGGATGAATCAATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766

Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 465
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-5

Query Match 48.5% Score 459; DB 10; Length 465;
Best Local Similarity 100.0% Pred. No. 1.3e-237;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 ATAAATACGATCACCCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 132
DB 4 ATAAATACGATCACCCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 63
QY 133 GAATCTCTTCTGTAATCAACGGAAGATCCAAACTAAATGCTATGCCATACCAATGCTA 192
DB 64 GAATCTCTTCTGTAATCAACGGAAGATCCAAACTAAATGCTATGCCATACCAATGCTA 123
QY 193 CCTGATACCTAATCGACCCCTTAAGTACTTATTGTTAAGCTCCAAAGTCCAAACCTTAAA 252
DB 124 CCTGATACCTAATCGACCCCTTAAGTACTTATTGTTAAGCTCCAAAGTCCAAACCTTAAA 183
QY 253 ACCATACCTAATCGTACGACCAATACTATACGCTGATGGCTATTCTGATCCCTTC 312
DB 184 ACCATACCTAATCGTACGACCAATACTATACGCTGATGGCTATTCTGATCCCTTC 243
QY 313 AATGGCAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
DB 244 AATGGCAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
QY 373 GTGGAGAACTACTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
DB 424 GGAATTCAAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
QY 553 AAACTAGGCTTTTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
DB 484 AAACTAGGCTTTTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 613 AAGTACATAGCAACCACTCAAGCTAATTTTAAATAGACATCTTACCTGATCCCAAA 572
DB 544 AAGTACATAGCAACCACTCAAGCTAATTTTAAATAGACATCTTACCTGATCCCAAA 603
QY 673 GTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 732
DB 604 GTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 563
QY 733 GGGGCTTTACCAACCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
DB 664 GGGGCTTTACCAACCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
QY 793 AGAGTGGATGAATCAATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
DB 724 AGAGTGGATGAATCAATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766

Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 465
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-5

Query Match 48.5% Score 459; DB 10; Length 465;
Best Local Similarity 100.0% Pred. No. 1.3e-237;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 ATAAATACGATCACCCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 132
DB 4 ATAAATACGATCACCCTTTGATGCTGGAATGCCACCATTAACAAATATGCCACCTTTATG 63
QY 133 GAATCTCTTCTGTAATCAACGGAAGATCCAAACTAAATGCTATGCCATACCAATGCTA 192
DB 64 GAATCTCTTCTGTAATCAACGGAAGATCCAAACTAAATGCTATGCCATACCAATGCTA 123
QY 193 CCTGATACCTAATCGACCCCTTAAGTACTTATTGTTAAGCTCCAAAGTCCAAACCTTAAA 252
DB 124 CCTGATACCTAATCGACCCCTTAAGTACTTATTGTTAAGCTCCAAAGTCCAAACCTTAAA 183
QY 253 ACCATACCTAATCGTACGACCAATACTATACGCTGATGGCTATTCTGATCCCTTC 312
DB 184 ACCATACCTAATCGTACGACCAATACTATACGCTGATGGCTATTCTGATCCCTTC 243
QY 313 AATGGCAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
DB 244 AATGGCAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
QY 373 GTGGAGAACTACTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
DB 424 GGAATTCAAATAGTCTGCTTCAAGTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
QY 553 AAACTAGGCTTTTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
DB 484 AAACTAGGCTTTTCTTCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 613 AAGTACATAGCAACCACTCAAGCTAATTTTAAATAGACATCTTACCTGATCCCAAA 572
DB 544 AAGTACATAGCAACCACTCAAGCTAATTTTAAATAGACATCTTACCTGATCCCAAA 603
QY 673 GTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 732
DB 604 GTAATTAATTTGGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 563
QY 733 GGGGCTTTACCAACCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
DB 664 GGGGCTTTACCAACCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
QY 793 AGAGTGGATGAATCAATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
DB 724 AGAGTGGATGAATCAATCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 766

Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 465
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-5

SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: Phytolacca americana
us-09-978-274A-7

Query Match
Best Local Similarity 100.0%; DB 10; Length 333;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 GGAGTTGATTCCTGCTGTAACAACTGAGCGCTTTTCTACTGGTAGCCATCCAAATG 591
Db 4 GGAGTTGATTCCTGCTGTAACAACTGAGCGCTTTTCTACTGGTAGCCATCCAAATG 63

QY 592 GTTTCAGAGCGAGCGGATTCAGTACATAGAGCAACCAAGTCAAGTCAATTTTATAGA 651
Db 64 GTTTCAGAGCGAGCGGATTCAGTACATAGAGCAACCAAGTCAAGTCAATTTTATAGA 123

QY 652 GCATTTCACCTGATCCCAAGTAATTAATTGAGGAGCAAGTGGGCAAAATCTCTGAG 711
Db 124 GCATTTCACCTGATCCCAAGTAATTAATTGAGGAGCAAGTGGGCAAAATCTCTGAG 183

QY 712 GCAATTCACAATGCCAAGATGGGCTTTTACCCAAACCACTTGGAGTGGATGCCAA 771
Db 184 GCAATTCACAATGCCAAGATGGGCTTTTACCCAAACCACTTGGAGTGGATGCCAA 243

QY 772 GTTACCAAGTGGATGCTTCTAGAGTGGATGAATCAATCGTATGTCGACCTCTTAAG 831
Db 244 GTTACCAAGTGGATGCTTCTAGAGTGGATGAATCAATCGTATGTCGACCTCTTAAG 303

QY 832 TAGCTTAATGGAACCTGTCAGACAACCTTA 860
Db 304 TAGCTTAATGGAACCTGTCAGACAACCTTA 332

RESULT 6
US-09-978-274A-15
Sequence 15, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 42
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PSXDF primer
US-09-978-274A-15

Query Match
Best Local Similarity 100.0%; DB 10; Length 42;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 GCTTTACCAACCACTTGGAGTGGATGCAAGGTACC 777
Db 1 GCTTTACCAACCACTTGGAGTGGATGCAAGGTACC 42

RESULT 7
us-09-978-274A-16/c
Sequence 16, Application US/09978274A

Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 42
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PSXDR primer
US-09-978-274A-16

Query Match
Best Local Similarity 100.0%; DB 10; Length 42;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GCGTTTACCAACCACTTGGAGTGGATGCAAGGTACC 776
Db 42 GCGTTTACCAACCACTTGGAGTGGATGCAAGGTACC 1

RESULT 8
US-09-978-274A-13
Sequence 13, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 52
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PS2BF primer
US-09-978-274A-13

Query Match
Best Local Similarity 100.0%; DB 10; Length 52;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 GGAGTTGATTCCTGCTGTAACAACTGAG 561
Db 23 GGAGTTGATTCCTGCTGTAACAACTGAG 52

RESULT 9
US-09-978-274A-31
Sequence 31, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard

APPLICANT: Neelam, Anil
 TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 FILE REFERENCE: 9341-028
 CURRENT APPLICATION NUMBER: US/09/978,274A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 0025225.4
 PRIOR FILING DATE: 2000-10-14
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 31
 LENGTH: 1368
 TYPE: DNA
 ORGANISM: Phytolacca americana
 US-09-978-274A-31

Query Match 3.1% Score 29; DB 10; Length 1368;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTTGTCATCTATTGAAGGATTCT 943
 DB 1136 TAATCTTGTCATCTATTGAAGGATTCT 1164

RESULT 10
 US-09-978-274A-30
 : Sequence 30, Application US/09978274A
 : Patent No. US20020116737A1
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Christopher
 : APPLICANT: McPherson, Michael
 : APPLICANT: Atkinson, Howard
 : APPLICANT: Neelam, Anil
 : TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 : FILE REFERENCE: 9341-028
 : CURRENT APPLICATION NUMBER: US/09/978,274A
 : CURRENT FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 0025225.4
 : PRIOR FILING DATE: 2000-10-14
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 30
 : LENGTH: 1379
 : TYPE: DNA
 : ORGANISM: Phytolacca americana
 US-09-978-274A-30

Query Match 3.1% Score 29; DB 10; Length 1379;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 TAATCTTGTCATCTATTGAAGGATTCT 943
 DB 1136 TAATCTTGTCATCTATTGAAGGATTCT 1164

RESULT 11
 US-09-978-274A-12/c
 : Sequence 12, Application US/09978274A
 : Patent No. US20020116737A1
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Christopher
 : APPLICANT: McPherson, Michael
 : APPLICANT: Atkinson, Howard
 : APPLICANT: Neelam, Anil
 : TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 : FILE REFERENCE: 9341-028
 : CURRENT APPLICATION NUMBER: US/09/978,274A
 : CURRENT FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 0025225.4
 : PRIOR FILING DATE: 2000-10-14
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn version 3.1

SEQ ID NO 12
 LENGTH: 47
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: PS2SR primer
 US-09-978-274A-12

Query Match 2.9% Score 27; DB 10; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 834 CGTTAATGGAACCTGTCAACACACITTA 860
 DB 47 CGTTAATGGAACCTGTCAACACACITTA 21

RESULT 12
 US-09-978-274A-14/c
 : Sequence 14, Application US/09978274A
 : Patent No. US20020116737A1
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Christopher
 : APPLICANT: McPherson, Michael
 : APPLICANT: Atkinson, Howard
 : APPLICANT: Neelam, Anil
 : TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 : FILE REFERENCE: 9341-028
 : CURRENT APPLICATION NUMBER: US/09/978,274A
 : CURRENT FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 0025225.4
 : PRIOR FILING DATE: 2000-10-14
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 14
 : LENGTH: 49
 : TYPE: DNA
 : ORGANISM: Unknown
 : FEATURE:
 : OTHER INFORMATION: PS1SR primer
 US-09-978-274A-14

Query Match 2.9% Score 27; DB 10; Length 49;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CTCACAGTCAGATTGGAATAATCTCT 531
 DB 49 CTCACAGTCAGATTGGAATAATCTCT 23

RESULT 13
 US-09-978-274A-11
 : Sequence 11, Application US/09978274A
 : Patent No. US20020116737A1
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Christopher
 : APPLICANT: McPherson, Michael
 : APPLICANT: Atkinson, Howard
 : APPLICANT: Neelam, Anil
 : TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 : FILE REFERENCE: 9341-028
 : CURRENT APPLICATION NUMBER: US/09/978,274A
 : CURRENT FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 0025225.4
 : PRIOR FILING DATE: 2000-10-14
 : NUMBER OF SEQ ID NOS: 32
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 11
 : LENGTH: 48
 : TYPE: DNA
 : ORGANISM: Unknown
 : FEATURE:

OTHER INFORMATION: PSIBF primer
US-09-978-274A-11

Query Match 2.8%; Score 26; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 ATAAATACGATCACCTTTGATGCTGG 98
Db 23 ATAAATACGATCACCTTTGATGCTGG 48

RESULT 14
US-09-978-274A-20/c
Sequence 20. Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 45
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PCS-PAPSR primer
US-09-978-274A-20

Query Match 2.6%; Score 25; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 CGTGATGTGGCACTCCTTAAGTACG 835
Db 45 CGTGATGTGGCACTCCTTAAGTACG 21

RESULT 15
US-09-978-274A-9
Sequence 9. Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 43
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PPSIBF primer
US-09-978-274A-9

Query Match 2.5%; Score 24; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGGTGATGCTTGTAGTTGTG 24
Db 20 ATGAAGGTGATGCTTGTAGTTGTG 43

Search completed: June 2, 2003, 05:53:35
Job time : 350 secs